

**PCT**WORLD INTELLECTUAL PROPERTY ORGANIZATION  
International Bureau

## INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification <sup>6</sup> : <b>A01N 63/00, 43/04, C12N 15/00, C07H 21/02</b>		<b>A1</b>	(11) International Publication Number: <b>WO 99/26480</b>
			(43) International Publication Date: 3 June 1999 (03.06.99)
(21) International Application Number: PCT/US98/24950			(81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, HR, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).
(22) International Filing Date: 20 November 1998 (20.11.98)			
(30) Priority Data: 08/975,424 20 November 1997 (20.11.97) US			
(71) Applicants: GENETIX PHARMACEUTICALS, INC. [US/US]: 840 Memorial Drive, Cambridge, MA 02139 (US). MASSACHUSETTS INSTITUTE OF TECHNOLOGY [US/US]: 77 Massachusetts Avenue, Cambridge, MA 02139 (US).			
(72) Inventors: LEBOULCH, Philippe; Flagship Warf, Unit 729, 197 8th Street, Charlestown, MA 02129 (US). PAWLIUK, Robert, James; Apartment 3, 52 Maple Avenue, Cambridge, MA 02129 (US). BACHELOT, Thomas; 53, rue Pierre Brunier, F-69300 Caluire (FR).			
(74) Agent: CLARK, Paul, T.; Clark & Elbing LLP, 176 Federal Street, Boston, MA 02110-2214 (US).			<b>Published</b> <i>With international search report.</i>
(54) Title: ANTI-ANGIOGENIC GENE THERAPY VECTORS AND THEIR USE IN TREATING ANGIOGENESIS-RELATED DISEASES			
(57) Abstract <p>A method for inhibiting tumor growth in a human patient harboring a solid tumor, said method comprising administering to said patient a nucleic acid molecule which expresses in said patient an anti-angiogenic polypeptide selected from the group consisting of human angiostatin, murine angiostatin, human endostatin, murine endostatin, and angiogenesis-inhibiting fragments thereof, wherein expression of the anti-angiogenic polypeptide in the patient inhibits angiogenesis in the vicinity of the tumor and/or systemically by diffusion of the recombinant protein to the vascular compartment from secreting transduced cells, thereby inhibiting its growth.</p>			

**FOR THE PURPOSES OF INFORMATION ONLY**

Codes used to identify States party to the PCT on the front pages of pamphlets publishing international applications under the PCT.

AL	Albania	ES	Spain	LS	Lesotho	SI	Slovenia
AM	Armenia	FI	Finland	LT	Lithuania	SK	Slovakia
AT	Austria	FR	France	LU	Luxembourg	SN	Senegal
AU	Australia	GA	Gabon	LV	Latvia	SZ	Swaziland
AZ	Azerbaijan	GB	United Kingdom	MC	Monaco	TD	Chad
BA	Bosnia and Herzegovina	GE	Georgia	MD	Republic of Moldova	TG	Togo
BB	Barbados	GH	Ghana	MG	Madagascar	TJ	Tajikistan
BE	Belgium	GN	Guinea	MK	The former Yugoslav Republic of Macedonia	TM	Turkmenistan
BF	Burkina Faso	GR	Greece	ML	Mali	TR	Turkey
BG	Bulgaria	HU	Hungary	MN	Mongolia	TT	Trinidad and Tobago
BJ	Benin	IE	Ireland	MR	Mauritania	UA	Ukraine
BR	Brazil	IL	Israel	MW	Malawi	UG	Uganda
BY	Belarus	IS	Iceland	MX	Mexico	US	United States of America
CA	Canada	IT	Italy	NE	Niger	UZ	Uzbekistan
CF	Central African Republic	JP	Japan	NL	Netherlands	VN	Viet Nam
CG	Congo	KE	Kenya	NO	Norway	YU	Yugoslavia
CH	Switzerland	KG	Kyrgyzstan	NZ	New Zealand	ZW	Zimbabwe
CI	Côte d'Ivoire	KP	Democratic People's Republic of Korea	PL	Poland		
CM	Cameroon	KR	Republic of Korea	PT	Portugal		
CN	China	KZ	Kazakhstan	RO	Romania		
CU	Cuba	LC	Saint Lucia	RU	Russian Federation		
CZ	Czech Republic	LI	Liechtenstein	SD	Sudan		
DE	Germany	LK	Sri Lanka	SE	Sweden		
DK	Denmark	LR	Liberia	SG	Singapore		
EE	Estonia						

ANTI-ANGIOGENIC GENE THERAPY VECTORS AND  
THEIR USE IN TREATING ANGIOGENESIS-RELATED DISEASES

5

Field of the Invention

This invention relates generally to gene therapy for, e.g., cancer.

Background of the Invention

Angiogenesis is the process by which new capillaries are formed from existing vasculature. It is a complex process which involves proliferation and migration of endothelial cells. It plays a fundamental role in reproduction, development and wound repair. Unregulated angiogenesis, however, can further the progression of many diseases, including tumor growth and metastasis, arthritis, diabetes, and some forms of blindness. For example, there is experimental evidence that limits of tumor size and growth are not the failure of the tumor cells to proliferate, but rather a failure of the tumor to provide sufficient nutrients and waste removal to its constituent cells by recruiting surrounding vasculature.

15

Summary of the Invention

The invention features a method for inhibiting tumor growth in a human patient harboring a solid tumor, involving administering to the patient a nucleic acid molecule which expresses in the patient an anti-angiogenic polypeptide selected from the group consisting of human angiostatin, murine angiostatin, human endostatin, murine endostatin, and angiogenesis-inhibiting fragments thereof, wherein expression of the anti-angiogenic polypeptide in the patient inhibits angiogenesis in the vicinity of the tumor and/or systemically by diffusion of the recombinant protein to the vascular compartment from secreting transduced cells, thereby inhibiting its growth.

20

25

In a second, related aspect, the invention features tumor inhibition, of

-2-

the type just described, using nucleic acids molecules of the formula A-B, where A and B are polypeptide and/or export signal joined by a peptide bond; peptide A contains at least 100 amino acids and includes at least kringles 1, 2, and 3 of human or murine angiostatin; and peptide B contains at least 100  
5 amino acids and includes at least 75% of the amino acid sequence of human or murine endostatin. Expression of the fusion anti-angiogenic polypeptide in the patient inhibits angiogenesis in the vicinity of the tumor and/or systemically by diffusion of the recombinant protein to the vascular compartment from secreting transduced cells, thereby inhibiting its growth. In some embodiments  
10 of this hybrid polypeptide and/or export signal method, polypeptide and/or export signal A further includes kringle region 4 of angiostatin, and can also include kringle region 5 of plasminogen (the larger protein molecule of which angiostatin is a portion).

In both aspects of the invention, the nucleic acid molecule preferably  
15 constitutes a portion of a viral vector or a plasmid, which can either be administered to the patient so that cells of the patient in the vicinity of the tumor and/or systemically by diffusion of the recombinant protein to the vascular compartment from secreting transduced cells are infected or transfected with the nucleic acid encoding the angiogenesis-inhibiting  
20 polypeptide, or cells (of the patient, or another human donor, or an animal) are infected or transfected *ex-vivo*, and those infected or transfected cells are then infused into the patient so that the anti-angiogenic polypeptide is expressed in the vicinity of the tumor and/or systemically by diffusion of the recombinant protein to the vascular compartment from secreting transduced cells.

25 As will be discussed in more detail below, in particularly effective embodiments, the nucleic acid molecule includes a nucleotide sequence

-3-

encoding a preactivation polypeptide and/or export signal for effecting Golgi and/or endoplasmic reticulum export of the anti-angiogenic polypeptide.

In another aspect, the invention features a method for treating a human patient suffering from diabetic retinopathy, involving administering to  
5 the patient one of the nucleic acid molecules described above.

The above and other features, objects and advantages of the present invention will be better understood by a reading of the following specification in conjunction with the drawings.

#### Brief Description of the Drawings

10 Fig. 1 depicts the structural relationship of angiostatin with plasminogen.

Fig. 2 depicts the structural relationship of endostatin with collagen type XVIII.

15 Fig. 3 depicts various viral (A. MSCV murine retrovirus; B. Adeno-associated virus; C. HIV based retrovirus; E. recombinant adeno-virus) and non-viral (D. plasmid) vectors used in the construction of gene therapy vectors for this invention.

-4-

## References:

- A. Hawley, R.G., F. H. L. Lieu, A. Z. C. Fong, and T. S. Hawley. 1994. Versatile retroviral vectors for potential use in gene therapy. *Gene Therapy* 1:136.
- B. Hargrove, P. H., E. F. Vanin, G. J. Kurtzman and A. W. Nienhuis. 1997. High-level globin gene expression mediated by a recombinant adeno-associated virus genome that contains a 3'  $\gamma$  globin gene regulatory element and integrates as tandem copies in erythroid cells. *Blood* 89:2167.
- C. Naldini, L., U. Blomer, P. Gallay, D. Ory, R. Mulligan, F. H. Gage, I. M. Verma, and D. Trono. 1996. In vivo gene delivery and stable transduction of nondividing cells by a Lentiviral vector. *Science* 272: 263.
- D.
- E. Ohashi, T., K. Watabe, K. Uehara, W. S. Sly, C. Vogler, and Y. Eto. 1997. Adenovirus-mediated gene transfer and expression of human  $\beta$ -glucuronidase gene in the liver, spleen, and central nervous system in mucopolysaccharide type VII mice. *PNAS* 94: 1287.

MSCV: Murine Stem Cell Virus  
 LTR: Long Terminal Repeat  
 RSV: Rous Sarcoma Virus  
 ITR: Inverted Terminal Repeat  
 HIV: Human Immunodeficiency Virus  
 IRES: Internal Ribosomal Entry Site  
 GFP: Green Fluorescence Protein  
 HBPRE: Hepatitis B Export Element  
 RRE: Rev Response Element  
 polyA: polyadenylation site  
 $\psi$ +: viral packaging sequence

The inverted triangle shows the site at which the anti-angiogenic constructs will be inserted using engineered MluI and XhoI restriction sites.

\* denotes specific mutations within the long terminal repeat and leader which bestows the ability for expression in embryonic stem and hematopoietic stem cells.

The arrow denotes the direction of transcription.

Fig. 4 depicts in the left (A) panel nude mice which were implanted with human neuroblastoma cells (line SK-N-AS) transduced with a mock virus and in the right (B) panel, nude mice which were transplanted with human neuroblastoma cells transduced with a retroviral gene therapy vector encoding an angiostatin-endostatin fusion protein.

Fig. 5 shows the nucleotide sequence (SEQ ID NO: 1) and amino

-5-

acid sequence (SEQ ID NO: 2) of human plasminogen and the nucleotide sequence (SEQ ID NO: 5) and amino acid sequence (SEQ ID NO: 6) of human angiostatin.

Fig. 6 shows the nucleotide sequence (SEQ ID NO: 9) and amino  
5 acid sequence (SEQ ID NO: 10) of murine endostatin.

Fig. 7 shows the nucleotide sequence (SEQ ID NO: 3) and amino acid sequence (SEQ ID NO: 4) of murine plasminogen and the nucleotide (SEQ ID NO: 7) and amino acid sequence (SEQ ID NO: 8) of murine angiostatin.

#### Detailed Description

10 This invention provides gene therapy using a vector having a nucleotide sequence encoding one of the above-identified anti-angiogenic polypeptides. Described below in more detail are some of the components of the vectors and methods of the invention.

By a gene therapy vector is meant a vector useful for gene therapy.  
15 Gene therapy vectors carry a gene of interest that is useful for gene therapy. The gene therapy vectors are able to be transferred to the cells of an animal, e.g., a human, and are able to express the gene of interest in such cells so as to effect gene therapy. The vector can be, e.g., chromosomal, non-chromosomal, or synthetic, and can be RNA or DNA. The vector can be, e.g., a plasmid, a  
20 virus or a phage. Preferred vectors include, e.g., retroviral vectors, adenoviral vectors, adeno-associated vectors, herpes virus vectors, Simliki Forest Virus-based vector, Human Immunodeficiency virus, Simian Immunodeficiency virus, and non-viral plasmids. A preferred retroviral vector is Murine Stem Cell Virus (MSCV), which is a variant of Moloney Murine Leukemia Virus  
25 (MoMLV).

By anti-angiogenic polypeptide is meant a polypeptide which inhibits

-6-

angiogenesis. The terms polypeptide, protein and polypeptide and/or export signal are used interchangeably herein. By angiogenesis is meant the process by which new vasculature, in particular, new capillaries, are formed from existing vasculature. Angiogenesis is a complex process entailing numerous steps, including local dissolution of the basement membrane, migration of endothelial cells into the surrounding stroma, proliferation of the endothelial cells at the leading edge to form a migrating column of cells, branching and fusion of the newly formed vascular loops, and formation of a new basement membranc. By inhibiting angiogenesis is meant completely or partially inhibiting the formation of such new vasculature.

In certain embodiments, the anti-angiogenic polypeptide is an anti-angiogenic fragment of plasminogen (in particular, angiostatin), an anti-angiogenic fragment of collagen XVIII (endostatin) or a fusion of the two fragments.

Angiostatin is an internal fragment of plasminogen having a molecular weight of 38 or 45 kDa, depending on whether it contains kringles 1-3 or 1-4. In the invention, either can be used, or a molecule including kringles 1-3 and a portion of kringle 4 can be used. Angiostatin can be naturally produced in vivo in small amounts by tumor cells, e.g. murine Lewis lung carcinoma cells, by proteolytic cleavage of plasminogen so as to eliminate the N-terminal portion including the signal polypeptide and/or export signal and the preactivation polypeptide and/or export signal, as well as the C-terminal portion following kringle 3 or 4. Mouse and human angiostatin have been purified and sequenced. In preferred embodiments, the gene therapy vectors of this invention encode angiostatin having kringles 1, 2 and 3, or angiostatin having kringles 1, 2, 3 and 4.

In another preferred embodiment, the anti-angiogenic polypeptide is



-7-

endostatin or a biologically active analog or fragment thereof. Endostatin can be naturally produced *in vivo* in small amounts by tumor cells, e.g., murine angiosarcoma cells, by proteolytic cleavage of endogenous collagen XVIII so as to eliminate the N-terminal portion including the signal polypeptide and/or  
5 export signal and the preactivation polypeptide and/or export signal, as well as the C-terminal portion following kringle 3 or 4. See Fig.2. Mouse endostatin has been sequenced, and the human molecule (SEQ ID NOs: 17 and 18) forms a portion of collagen 18 (SEQ ID NOs: 19 and 20).

The human molecule position and sequence are apparent from an  
10 alignment of the active, Lys-terminated active region of human collagen 18 with murine endostatin, such that the C-terminal lysine residues align, bringing the active endostatin sequences into alignment.

In yet another preferred embodiment, the anti-angiogenic polypeptide is an in-frame fusion of angiostatin or a biologically active analog  
15 or fragment thereof and endostatin or a biologically active analog or fragment thereof. Preferably, the angiostatin or biologically active analog or fragment is 5' of the endostatin or biologically active analog or fragment. In certain embodiments, the angiostatin-endostatin fusion proteins exhibit synergistic anti-angiogenic properties.

20 By fragment is meant some portion of the naturally occurring anti-angiogenic polypeptide. Preferably, the fragment is at least 20 amino acid residues, more preferably at least 50 amino acid residues, and most preferably at least 100 amino acid residues in length. Fragments include chimeric constructs composed of at least a portion of the relevant gene and another  
25 molecule. The ability of a candidate fragment to exhibit a biological activity of the anti-angiogenic polypeptide can be assessed by methods known to those skilled in the art, e.g., by its ability to inhibit proliferation of bovine capillary

-8-

cells, or by its ability to inhibit growth of primary tumor cells, e.g., as described herein. See, e.g., Example 9. Also included are fragments containing residues that are not required for biological activity of the fragment or that result from alternative mRNA splicing or alternative protein processing events.

5           Internal or terminal fragments of a polypeptide can be generated by removing one or more nucleotides from one end (for a terminal fragment) or both ends (for an internal fragment) of a nucleic acid which encodes the polypeptide.

          In preferred embodiments, the gene therapy vector of this invention is  
10   capable of hybridizing to the native anti-angiogenesis polypeptide-encoding regions and has at least about 80%, preferably at least about 90%, and more preferably at least about 95%, sequence identity to the native nucleotide sequences, and encodes a polypeptide which has anti-angiogenic activity; or a biologically active fragment of any of the above nucleotide sequences wherein  
15   the encoded polypeptide has anti-angiogenic activity.

          The nucleotide sequences of the present invention can be in the form of RNA or DNA, and the nucleotide sequence can be double-stranded or single stranded and, if single stranded, can be the coding strand or non-coding (anti-sense) strand.

20           The coding sequence which encodes the anti-angiogenic polypeptide can be identical to the native coding sequences, or can be a different coding sequence which, as a result of the degeneracy of the genetic code, encodes the same anti-angiogenic polypeptide.

          In certain embodiments, the gene therapy vector also has a nucleotide  
25   sequence encoding a signal polypeptide and/or export signal (SP) for effecting secretion of the anti-angiogenic polypeptide. Examples of signal polypeptide and/or export signal include plasminogen signal polypeptide and/or export

-9-

signal. Preferably, the signal polypeptide and/or export signal is 5' (i.e., upstream) of the nucleotide sequence encoding the anti-angiogenic polypeptide.

Preferably, the gene therapy vector has a nucleotide sequence encoding a preactivation polypeptide and/or export signal (PAP), which is a small  
5 polypeptide and/or export signal which effects folding and secretion of the anti-angiogenic polypeptide *in vivo*. Examples of preactivation polypeptide and/or export signal include plasminogen preactivation polypeptide and/or export signal, described herein, and PAP's of other proteins in the blood clotting cascade.

10 Preferably, the preactivation polypeptide and/or export signal is positioned 5' of the nucleotide sequence encoding the anti-angiogenic polypeptide. In embodiments which have a signal sequence and an anti-angiogenic polypeptide, preferably the preactivation polypeptide and/or export signal is 5' of the nucleotide sequence encoding the anti-angiogenic  
15 polypeptide, and 3' of the nucleotide sequence encoding the signal polypeptide and/or export signal.

We have discovered that results obtained using constructs containing a PAP- encoding nucleic acid sequence are far superior to results using constructs lacking a PAP-encoding sequence. Our hypothesis to explain these  
20 unexpectedly superior results with PAP is that, during the complex process by which the anti-angiogenic polypeptide is expressed and processed in living cells, the PAP polypeptide and/or export signal facilitates the export of the polypeptide from the cellular Golgi apparatus and/or the endoplasmic reticulum (ER). The corollary is that, absent PAP, a significant portion of the expressed  
25 polypeptide remains trapped in the Golgi and/or ER.

The PAP exemplified herein is derived from human plasminogen; this

-10-

PAP is currently preferred. Our discovery that the use of a PAP dramatically improves results leads us to believe that other PAP's would be useful as well, and such others are therefore contemplated for use in the invention. Thus, as used herein, "PAP" refers to a polypeptide and/or export signal which is

5 naturally associated with a eukaryotic (preferably human) protein, the exportation of which is facilitated by its associated PAP. Examples of other human proteins whose Golgi/ER export is PAP-facilitated include other secreted proteins of the blood coagulation cascade, e.g., fibrinogen, prothrombin, Factor VIII, and Factor IX. Other secreted human proteins also

10 are associated with potentially useful PAPs.

It is not essential that the PAP used in the invention be identical in amino acid sequences to a native PAP; it is well-known that polypeptide and/or export signal that facilitate protein secretion or export, e.g., signal polypeptide and/or export signal and PAPs, can vary from the native forms to a certain

15 extent and still retain their function. Therefore, PAPs useful according to the invention preferably have 75% or greater amino acid sequence identity with a native PAP.

In certain embodiments, the gene therapy vector has a nucleotide sequence encoding a tag for identification of the anti-angiogenic polypeptide

20 and/or export signal. In certain embodiments, the tag is 5' of the nucleotide sequence encoding the anti-angiogenic polypeptide; in other embodiments, the tag is 3' of the nucleotide sequence encoding the anti-angiogenic polypeptide. In embodiments in which the anti-angiogenic polypeptide is endostatin or an angiostatin-endostatin fusion, it is preferred that the tag be 5' of the nucleotide

25 sequence encoding endostatin.

In certain embodiments the gene therapy vector includes a selectable

-11-

marker, e.g., a Neomycin phosphotransferase gene, or a humanized red-shifted green fluorescent protein.

The invention also includes a cell infected or transfected with a gene therapy vector described herein. Preferably, the cell is an animal cell, more preferably an autologous or allogeneic human cell. The gene therapy vectors  
5 described herein can be introduced into a cell, e.g., by transformation, transfection, transduction, infection, or ex vivo injection. They can be targeted to a particular cell type.

Administration of nucleic acid, e.g., a gene therapy vector, can be  
10 accomplished by any method which allows the nucleic acid to reach the target cells. These methods include, e.g., injection, deposition, implantation, suppositories, oral ingestion, inhalation, topical administration, or any other method of administration where access to the target cells by the nucleic acid is achieved. Injections can be, e.g., intravenous, intradermal, subcutaneous,  
15 intramuscular or intraperitoneal. Implantation includes inserting implantable drug delivery systems, e.g., microspheres, hydrogels, polymeric reservoirs, cholesterol matrices, polymeric systems, e.g., matrix erosion and/or diffusion systems and non-polymeric systems, e.g., compressed, fused or partially fused pellets. Suppositories include glycerin suppositories. Oral ingestion doses can  
20 be enterically coated. Inhalation includes administering the nucleic acid with an aerosol in an inhalator, either alone or attached to a carrier that can be absorbed.

In certain embodiments of the invention, administration can be designed so as to result in sequential exposures to the nucleic acid over some time  
25 period, e.g., hours, days, weeks, months or years. This can be accomplished by repeated administrations of the nucleic acid, e.g., by one of the methods described above, or alternatively, by a controlled release delivery system in

-12-

which the nucleic acid is delivered to the animal over a prolonged period without repeated administrations. By a controlled release delivery system is meant that total release of the nucleic acid does not occur immediately upon administration, but rather is delayed for some time. Release can occur in bursts  
5 or it can occur gradually and continuously. Administration of such a system can be, e.g., by long acting oral dosage forms, bolus injections, transdermal patches or subcutaneous implants. Examples of systems in which release occurs in bursts include, e.g., systems in which the nucleic acid is entrapped in liposomes which are encapsulated in a polymer matrix, the liposomes being  
10 sensitive to a specific stimulus, e.g., temperature, pH, light, magnetic field, or a degrading enzyme, and systems in which the nucleic acid agent is encapsulated by an ionically-coated microcapsule with a microcapsule core-degrading enzyme. Examples of systems in which release of the nucleic acid is gradual and continuous include, e.g., erosional systems in which the nucleic acid is  
15 contained in a form within a matrix, and diffusional systems in which the nucleic acid permeates at a controlled rate, e.g., through a polymer. Such sustained release systems can be, e.g., in the form of pellets or capsules.

The nucleic acid is administered to the patient in a therapeutically effective amount. By therapeutically effective amount is meant that amount  
20 which is capable of at least partially preventing or reversing the disease. A therapeutically effective amount can be determined on an individual basis and will be based, at least in part, on consideration of the patient's size, age, the efficacy of the particular nucleic acid used, the type of delivery system used, the time of administration relative to the onset of disease symptoms, and  
25 whether a single, multiple, or controlled release dose regimen is employed. A therapeutically effective amount can be determined by one of ordinary skill in the art employing such factors and using no more than routine experimentation.

-13-

In certain embodiments, a therapeutically effective amount of an anti-angiogenic polypeptide is administered by providing to the animal a nucleic acid encoding the polypeptide and expressing the polypeptide in vivo. Nucleic acids encoding the polypeptide, or mutants thereof, can be administered in any  
5 biologically effective carrier, e.g. any formulation or composition capable of effectively delivering the nucleotide sequence for the anti-angiogenic polypeptide to cells in vivo. Approaches include, e.g., insertion of the nucleic acid into viral vectors. Viral vectors can be delivered to the cells, e.g., by infection or transduction using the virus. Viral vectors can also be delivered to  
10 the cells, e.g., by physical means, e.g., by electroporation, lipids, cationic lipids, liposomes, DNA gun,  $\text{Ca}_3(\text{PO}_4)_2$  precipitation, or delivery of naked DNA. In certain preferred embodiments, the virus is administered by injection, e.g., intramuscular injection, in a dose range of about  $10^3$  to about  $10^{10}$  infectious particles per injection, more preferably in a dose range of about  $10^5$  to about  
15  $10^8$  infectious particles per injection. Single or multiple doses can be administered over a given period of time, depending, e.g., upon the disease.

An alternative is insertion of the nucleic acid encoding the anti-angiogenic polypeptide into a bacterial or eukaryotic plasmid. Plasmid DNA can be delivered to cells with the help of, e.g., cationic liposomes (lipofectin™;  
20 Life Technologies, Inc., Gaithersburg, MD) or derivatized (e.g., antibody conjugated) polylysine conjugates, gramicidin S, artificial viral envelopes or other such intracellular carriers, as well as direct injection of the gene construct or  $\text{Ca}_3(\text{PO}_4)_2$  precipitation carried out in vivo, or by use of a gene gun. The above-described methods are known to those skilled in the art and can be  
25 performed without undue experimentation.

Since transfer of the nucleic acid to appropriate target cells represents the critical first step in gene therapy, choice of the particular gene delivery

-14-

system will depend on such factors as the intended target and the route of administration, e.g., locally or systemically. Targets for delivery of the nucleic acid can be, e.g., specific target cells which are diseased. For example, the target can be, e.g., the peritoneal cavity, gastro-intestinal tract, bone marrow  
5 cavity, liver, lungs, muscles, vasculature, pericardial cavity, pleural cavity, skin, sub-cutaneous or deep connective tissues, central nervous system, spinal fluid, eye, or specific sites of tumor growth. Administration can be directed to one or more cell types, and to one or more cells within a cell type, so as to be therapeutically effective, by methods known to those skilled in the art. For  
10 example, the nucleic acid can be, e.g., coupled to an antibody, to a ligand to a cell surface receptor, or to a toxin component, or can be contained in a particle which is selectively internalized into cells, e.g., liposomes, or a virus where the viral receptor binds specifically to a certain cell type, or a viral particle lacking the viral nucleic acid, or can be administered by local injection.

15 In certain embodiments, the nucleic acid is administered to the patient by introducing *ex vivo* the nucleic acid into cells of the patient, or into syngeneic or allogeneic or xenogeneic cells, and then administering the cells having the nucleic acid to the animal. Any cell type can be used. In certain embodiments, the cells having the introduced nucleic acid are expanded and/or  
20 selected after the nucleic acid transfer. The cells having the transferred nucleic acid are subsequently administered to the patient. Preferably, the cells are administered in a dose range of about  $1 \times 10^6$  to about  $1 \times 10^9$  cells/dosage/day, and most preferably at about  $1 \times 10^7$  to about  $1 \times 10^8$  cells/dosage/day. The cells can be administered by any method which results in delivering the  
25 transferred nucleic acid in the cells to the desired target. For example, the cells can be implanted directly into a specific tissue of the patient, or implanted after encapsulation within an artificial polymer matrix. Examples of sites of



-15-

implantation include, e.g., the peritoneal cavity, gastro-intestinal tract, bone marrow cavity, liver, lungs, muscles, vasculature, pericardial cavity, pleural cavity, skin, sub-cutaneous or deep connective tissues, central nervous system, spinal fluid, eye, or specific sites of tumor growth.

5           Systemic delivery can be achieved, e.g., by introducing the nucleic acid into cells which circulate in the peripheral blood of the patient, or which give rise to cells which circulate in the peripheral blood. In certain embodiments, the nucleic acid is introduced into such cells *ex vivo*, and these cells are then administered to the patient, resulting in systemic delivery within the peripheral  
10   blood. These cells can be the cells of the patient or allogeneic cells. Preferred cells in which the nucleic acid can be introduced are hematopoietic cells.

          In certain embodiments, other therapy is additionally administered. For example, if the animal is being treated for a tumor, other tumor therapy, e.g., another therapeutic agent, chemotherapy, radiation or surgery, is additionally  
15   administered to the patient, either simultaneously or at different times.

          Treating is meant to include, e.g., preventing, treating, reducing the symptoms of, or curing the disease. I.e. treating a tumor includes preventing growth of the tumor, causing shrinkage of the tumor, or preventing development of micro-metastases.

20           Preferably, the recombinant nucleic acid is a gene therapy vector, e.g., as described herein. Preferably, the anti-angiogenic polypeptide is angiostatin, endostatin, an angiostatin-endostatin fusion protein, or biologically active analogs or fragments thereof. In certain embodiments, the angiostatin has kringles 1, 2 and 3; in other embodiments, the angiostatin has kringles 1, 2, 3  
25   and 4, and, in some embodiments, kringle 5 of human or murine plasminogen. Angiostatin is described in O'Reilly and Folkman U.S. Patent No. 5,639,725, hereby incorporated by reference. Endostatin is described in O'Reilly and

-16-

Folkman PCT Appln. No. WO 97/15666, published May 1, 1997, hereby incorporated by reference.

In certain embodiments, the recombinant nucleic acid has been introduced *ex vivo* into cells so as to express the anti-angiogenic polypeptide in the cells, and the recombinant nucleic acid is administered to the patient by administering to the patient the cells containing the recombinant nucleic acid. In certain embodiments, the cells are derived from the patient; in other embodiments the cells are allogeneic cells relative to the cells of the patient.

Where cells are infected or transfected *ex vivo* for later infusion into the patient, the cells are preferably hematopoietic cells, but can also be mesenchymal cells, stem cells, epithelial cells (e.g., from the gut), or dendritic cells.

The gene therapy vectors of the invention can be provided in a pharmaceutical composition comprising a therapeutically effective amount of the recombinant nucleic acid together with a pharmaceutically acceptable carrier. Pharmaceutically acceptable carriers include, e.g., water, saline, dextrose, glycerol, ethanol, liposomes and lipid emulsions.

The following non-limiting examples further illustrate the present invention.

20

#### EXAMPLES

Example 1: Construction of Inserts for Gene Therapy Vectors Containing cDNA for Angiostatin, Endostatin or Angiostatin-Endostatin Fusion Proteins

The following genetic constructs are inserted into retroviral gene therapy vectors; the genetic constructs contain human or murine cDNA for angiostatin, endostatin or an angiostatin-endostatin fusion, and DNA encoding a signal

-17-

polypeptide and/or export signal (SP), a tag (FLAG), and, preferably, a preactivation polypeptide and/or export signal (PAP). The constructs are all made using standard genetic engineering techniques, and their insertion into retroviral gene therapy vectors is carried out using known methods. The

5 constructs have the following components:

Murine Constructs

SP-K1-K2-K3-Flag  
SP-K1-K2-K3-K4-Flag  
SP-K1-K2-K3-K4-K5-Flag  
10 SP-PAP-K1-K2-K3-Flag  
SP-PAP-K1-K2-K3-K4-Flag (SEQ ID NO: 11 and 12)  
SP-Flag-Endo (SEQ ID NO: 13 and 14)  
SP-K1-K2-K3- Flag-Endo  
SP-K1-K2-K3-K4- Flag-Endo (SEQ ID NO: 15 and 16)  
15 SP-PAP-K1-K2-K3- Flag-Endo

Human Constructs

SP-K1-K2-K3  
SP-K1-K2-K3-K4  
SP-K1-K2-K3-K4-K5  
20 SP-PAP-K1-K2-K3  
SP-PAP-K1-K2-K3-K4  
SP-PAP-K1-K2-K3-K4-K5  
SP-Endo  
SP-K1-K2-K3-Endo  
25 SP-PAP-K1-K2-K3-Endo

Nucleic acid and amino acid sequences for mouse and human angiotensin and endostatin used in these constructs are shown in Figs. 5-7.

Nucleic acid and amino acid sequence of the FLAG peptide:

amino terminus-	ASP	TYR	LYS	ASP	ASP	ASP	ASP	LYS
5'-	GAC	TAC	AAG	GAC	GAC	GAT	GAC	AAG

#### Human plasminogen derivative constructs

The entire coding region of the human plasminogen cDNA from the start (ATG) to the stop (TAA) codon is 2433bp in size.

This sequence encodes a signal peptide (bp 1-57), a preactivation peptide (bp 58-288), and 5 distinct structural regions known as kringles (K1-K3 from bp 289-1092; K4 from bp 1093-1380; K5 from bp 1381-1740). Please note that although I have given precise bp measurements for kringles K4 and K5, it can be argued that the sequence encoding K4 is between bp 1056-1440 and the sequence encoding K5 is between bp 1362-1680.

A DNA fragment encoding a portion of the human plasminogen protein from bp 1 to 1377 was obtained by PCR of a widely available human liver cDNA library using synthetic DNA oligonucleotides complementary to sequences immediately preceding the signal peptide and immediately following kringle 4. This fragment contains the signal peptide (bp 1-57), the preactivation peptide (bp 58-288), kringles 1 (bp 289-549), 2 (bp 550-804), 3 (bp 805-1092) and 4 (bp 1093-1380). The synthetic oligonucleotides used for this reaction contained engineered recognition sites for the restriction enzymes EcoRI and XhoI. Following the PCR reaction the amplified fragment was cloned into the EcoRI/XhoI sites of BluescriptSK(-) (Stratagene) using standard techniques (Maniatis). Following cloning the integrity of the amplified sequence was verified by sequencing both strands using the Sanger method (Sanger). Various derivatives of the cloned fragment were subsequently constructed using BluescriptSK(-) (Stratagene) as a backbone. A full list of the derivatives are described in Table 1. Briefly, the variations are composed of constructs containing various combinations of kringles with or without the signal and/or preactivation peptide sequences. These derivatives were constructed using both standard techniques as well as PCR and the use of double stranded synthetic oligonucleotides. In all cases the integrity of the start codon, coding sequence and termination codon was verified by double stranded sequencing using the Sanger method.

#### Murine plasminogen derivative constructs

The coding sequence for murine plasminogen is 2439bp in size and, similar to the human plasminogen cDNA encompasses a sequence encoding signal and preactivation peptides (bp 1-57 and 58-288 respectively) in addition to 5 kringle regions; kringle 1-3 (bp 289-1092), kringle 4 (bp 1093-1380) and kringle 5 (bp 1381-1743). Again, although I have given precise bp measurements for kringles K4 and K5, it can be argued that the sequence encoding K4 is between bp 1056-1440 and the sequence encoding K5 is between bp 1362-1680.

The murine plasminogen cDNA has previously been cloned and was made available to us. Derivatives of murine plasminogen were constructed using sequences derived from bp 1-1743 of the coding sequence. Various combinations of kringle regions with or without signal and preactivation peptide regions were made using BluescriptSK(-) (Stratagene, La Jolla, CA) as the vector backbone. These derivatives were constructed using standard cloning techniques (Maniatis, Molecular cloning; a laboratory manual, second edition, 1989) in combination with PCR utilizing synthetic oligonucleotides using

-19-

Angiostatin function was not altered by adding the FLAG polypeptide and/or export signal to either the N- or C-terminal ends, whereas endostatin was functional only if FLAG was added to its N-terminal end.

Example 2: Construction of Retroviral Gene Therapy Vectors

5 This example illustrates the construction of retroviral gene therapy vectors comprising cDNA for angiostatin, endostatin or angiostatin-endostatin fusion proteins.

The DNA inserts from Example 1 were inserted into two retroviral vectors. Both vectors were derived from the Murine Stem Cell Virus (MSCV),  
10 which is a variant of Moloney Murine Leukemia Virus (MoMLV) having several mutations allowing high, sustained expression in hematopoietic stem cells and their progeny. In both cases, the angiostatin, endostatin, or angiostatin-endostatin fusion DNA inserts were under the transcriptional control of the retroviral left Long Terminal Repeat (LTR). In the first vector,  
15 the dominant selectable marker was the Neomycin phosphotransferase gene (NeoR), which confers resistance to G418, and is driven by an internal phosphoglycerate kinase (PGK) promoter. In the second vector, the dominant selectable marker was the humanized, red-shifted green fluorescent protein (EGFP), which is co-translationally expressed by means of an Internal  
20 Ribosome Entry Site (IRES) from the Encephalomyocarditis virus (EMCV).

The retroviral gene therapy vectors were transfected by  $\text{CaPO}_4$  precipitation in the transient ecotropic packaging cell-line BOSC 23, Pear et al., *PNAS* 90:8392 (1993). Viral supernatants were collected two days thereafter and filtered through 0.45 mm filters. Filtered viral supernatants were  
25 subsequently used to infect GENETIX's stable amphotropic retroviral packaging cell-line AM12 (Genetix Pharmaceuticals, Inc., Cambridge, MA). After another two days, viral supernatants from transduced AM12 were filtered

-20-

and used to infect GENETIX's stable ecotropic retroviral packaging cell-line GP+E86 (Genetix Pharmaceuticals, Inc.). Both transduced AM12 and GP+E86 were then selected in the presence of G418 (in the case of constructs bearing NeoR) or sorted by Fluorescent Activated Cell Sorter (FACS) for EGFP expression. Viral titers were estimated according to standard practice by counting G418 resistant colonies among NIH3T3 cells exposed to diluted virus preparation. Ecotropic viral titers were above  $5 \times 10^5$  /ml of viral supernatants, only 3-fold lower than "empty" control vectors. No Replication Competent Retrovirus (RCR) was detected in standard assays.

10 Example 3: Transduction of Target Cells Using Retroviral Gene Therapy Vectors

This example illustrates the stability of retroviral gene therapy vector transmission and the lack of toxicity in non-endothelial target cells.

Following 24-hour incubation of confluent viral producer cells in 100 mm plates, viral supernatant was removed and filtered (0.45  $\mu$ m filter, Gelman Sciences, Ann Arbor, MI). Viral supernatant, containing 7  $\mu$ g/ml polybrene (Sigma, St. Louis, MO), was added to target cells 24 hours after plating the target cells. Fresh medium was added after 4-12 hours, and, after an additional 48 hours, cells were selected for retroviral infection by exposure to medium containing 1 mg/ml G418 (Gibco BRL, Grand Island, NY) or by FACS sorting (FACStar cell sorter, Becton Dickinson, San Jose, CA). The stability of transmission of the retroviral gene therapy vectors described in Example 2 was examined by Southern blot analysis of transduced NIH3T3 cells, using specific probes (EGFP) and restriction enzyme digestion of genomic DNA with SacI, which cuts only once in each LTR. Stable chromosomal integration of intact proviruses of appropriate length was observed with all constructs.

The lack of non-specific toxicity on non-endothelial cells was

-21-

established by using filtered viral supernatants to transduce various tumor cell-types and cell-lines (NIH3T3 cells, K562 cells (ATCC), and human SK-N-AS neuroblastoma cells; Cohen, P.S., *Cancer Research*, 55:2380 (1995).

Transduced cell populations were subsequently selected with G418 or sorted  
5 for EGFP expression by FACS. No obvious effects on cell viability, growth or other phenotypical characteristics were detected.

Example 4: Protein Expression of Angiostatin, Endostatin and Angiostatin-Endostatin Fusion Proteins in Cells Transduced with Retroviral Gene Therapy Vectors

10 This example illustrates that recombinant angiostatin, endostatin, and angiostatin-endostatin fusion proteins were readily detected in retrovirally transduced cells and their supernatant, indicating efficient expression and secretion.

MSCV virus based vectors containing sequences encoding murine  
15 Kringle 1 (K1), K1K5, K1K2K3, K1K2K3K4, and K1K2K3K4K5 were used to transduce NIH3T3 cells. With regard to the murine recombinant proteins, Western blot analysis of transduced cells and their supernatant was performed by means of a monoclonal antibody that recognizes the FLAG polypeptide and/or export signal. Because this antibody is not mono-specific, significant  
20 cross-reactivity with murine proteins was apparent. However, by comparing the pattern obtained with mock cells, it was clear that the antibody revealed an additional band of appropriate size in all transduced cells. Moreover, the recombinant proteins were detected in cell supernatants at levels above 50 ng/ml, using a protein concentration/semi-purification procedure (Centricon  
25 columns, Amicon, Beverly, MA). With regard to the human recombinant proteins, no FLAG tag was added, so a monoclonal antibody that recognizes specifically the first three kringles of human plasminogen in its native, non-

-22-

denatured form was used; O'Reilly et al., *Cell* 79:315 (1994). Because of this constraint, Western blot analysis using denaturing gels could not be performed. An ELISA assay was performed which indicated that human recombinant angiostatin was detected at levels likely to be therapeutic according to previous  
5 findings in the model of Lewis Lung Carcinoma *Id.*

These results indicate that high levels of recombinant proteins of expected length were expressed in retrovirally transduced cells and were efficiently secreted.

10 Example 5: In Vivo Anti-Tumor Activity of Cells Transduced with Gene Therapy Vectors Encoding the Angiostatin-Endostatin Fusion Protein

Human SK-N-AS neuroblastoma cells (Cohen, 1995) were transduced with the retroviral gene therapy vector containing the angiostatin-endostatin fusion protein, described in Example 2. These cells (1,000,000) were  
15 suspended in 1 mL Dulbecco's phosphate buffered saline and injected into the right mid-quadrant of nude immuno-compromised mice. While no impairment of the *in vitro* growth of transduced cells was observed, a dramatic decrease in tumor growth in nude mice cells following subcutaneous implantation of the transduced cells was evident as compared to "mock virus"-transduced control  
20 cells.

Example 6: Ex Vivo Transfer of Retroviral Gene Therapy Vectors Encoding Anti-Angiogenic Polypeptides to Primary Hematopoietic Cells, and Subsequent Transplantation to Recipient Mice

This example illustrates infection of primary hematopoietic cells from



-23-

donor mice with retroviral gene therapy vectors encoding angiostatin, endostatin, or an angiostatin-endostatin fusion protein, and a selectable GFP marker, and subsequent transplantation of the transduced hematopoietic cells into recipient mice.

- 5           Femoral bone marrow cells are harvested from male donor C57BL6/J-Ly5.1 mice (Jackson Labs, Bar Harbor, ME), intravenously injected four days previously with 150 mg/kg of 5-fluorouracil (5-FU). Bone marrow cells are cultured for two days in medium composed of DMEM, 15% fetal calf serum, 10 ng/ml human IL-6, 6 ng/ml murine IL-3 and 100 ng/ml murine Steel factor
- 10 prior to two days of culture atop a confluent monolayer of irradiated (1,500 cGy, <sup>137</sup>Cs γ-irradiation) viral producer cells in the above medium including 6 ug/ml of prolamine sulfate. The viral producer cells are transfected with a retroviral gene therapy vector, as described above. Upon completion of the co-culture infection protocol, recovered non-adherent cells are cultured for an
- 15 additional 48 hours to allow for expression of the transferred GFP gene. Retrovirally transduced cells expressing the transferred GFP gene are subsequently identified and selected for, using a FACStar+ cell sorter (Becton Dickinson, San Jose, CA). The GFP+ cells are intravenously injected into congenic female C57BL6/J-Ly5.2 recipient mice (National Cancer Institute,
- 20 Washington, DC) previously given 950 cGy (83cGy/min, <sup>137</sup>Cs γ-rays) of whole body irradiation. In each case, a small fraction of GFP+ sorted cells is used for day 12 CFU-S and in vitro clonogenic progenitor assays to assess the efficiency of the infection and selection procedures on these more mature cell types.

25   Example 7: Engraftment of Recipient Mice with Donor-Derived Hematopoietic Cells

This example illustrates engraftment of the recipient mice with the

-24-

donor-derived transfected hematopoietic cells from Example 6.

The donor and recipient mice are phenotypically distinguishable on the basis of Y chromosome specific sequences, as well as on the basis of allelic differences at the murine CD45 cell surface antigen locus. Male donor mice are homozygous for the CD45.2 allele, while female recipient mice are homozygous for CD45.1. The engraftment of recipient mice with donor-derived (CD45.2+) cells is assessed at both short (5 weeks) and long (34 months) time points post-transplant by flow cytometric analysis of peripheral blood samples stained with a phycoerythrin labeled antibody specific for the CD45.2 antigen (Pharmingen, San Diego, CA). The results indicate that engraftment occurs.

Example 8: Proviral Marking and GFP Expression in Recipient Mice

This example illustrates the presence of recombinant provirus and expression of the transferred GFP gene in the recipient mice from Example 6.

The level of proviral marking in reconstituted animals is initially determined by Southern blot and semi-quantitative PCR analysis of DNA obtained from peripheral blood leukocytes. The large majority of donor-derived (CD45.2+) cells in recipient mice contain a minimum of one copy of recombinant provirus. In addition, flow cytometric analysis of peripheral blood leukocytes is performed to ascertain the proportion of cells expressing the transferred GFP cDNA. Because the GFP and angiogenic inhibitor protein cDNAs are both driven from the same regulatory sequences, due to the inclusion of an internal ribosomal entry site (IRES) element, the analysis of GFP expression in the peripheral blood provides an indirect measurement of the levels of anti-angiogenic protein being expressed. The results indicate expression of the transferred genes.

Example 9: Anti-Angiogenic Polypeptide Expression in Recipient Mice

This example illustrates the presence of anti-angiogenic polypeptide in the sera of the recipient mice from Example 6, using both physical and functional assays.

5           Serum obtained from the transplanted animals described in Example 6 is used for ELISA using an antibody specific for the synthetic FLAG epitope (IBI, Eastman Kodak, New Haven, CT) and compared against known standards of purified protein. Results indicate the presence of the anti-angiogenic polypeptide in the serum.

10           To determine whether a functional anti-angiogenesis polypeptide is present in the circulation, sera from transplanted animals is tested for its ability to inhibit the proliferation of bovine capillary cells *in vitro*; O'Reilly (1994). Briefly, cells are plated in 24 well dishes at 25,000 cells/ml and maintained in DMEM with 5% bovine calf serum for 24 hours. The medium is then replaced  
15           with fresh medium containing various dilutions of the test serum. After 20 minutes of incubation, fresh medium including b-FGF (final concentration 1 ng/ml) is added and the cells are cultured for 72 hours. Cells are then dispersed using trypsin and the cell number determined by Coulter counter. Results indicate that functional anti-angiogenic polypeptide is present in the sera of the  
20           recipient mice.

            In addition, the ability of circulating anti-angiogenic polypeptide to inhibit the growth of primary tumor cells is assessed. Transplanted mice are subcutaneously injected with one million Lewis lung carcinoma (LLC) cells (O'Reilly, (1994)) at the proximal midline of their dorsal skin. The mice are  
25           closely monitored for survival, tumor size and growth, and overall health. Results indicate that the anti-angiogenic polypeptides from the sera of the

-26-

recipient mice inhibit growth of the LLC tumor cells.

Finally, upon sacrifice of the transplanted recipient mice, blood, spleen, thymus and bone marrow are harvested and analyzed for the presence of proviral DNA by Southern analysis as well as expression of the transferred

5 GFP and anti-angiogenic polypeptide cDNAs by flow cytometry and ELISA. Moreover, a portion of bone marrow cells is re-transplanted into secondary recipients to generate individual day 12 spleen colonies, as well as plated in methylcellulose to assess *in vitro* clonogenic progenitors. Individual clones are analyzed for proviral DNA by PCR or Southern blot, and for gene expression

10 by flow cytometry and ELISA. Results of these tests also indicate the presence of proviral DNA and expression of the anti-angiogenic polypeptides and marker proteins.

15 Example 10: Evaluating the Efficacy of Retroviral Gene Therapy Vectors Encoding Anti-Angiogenic Polypeptides on Various Human Cancers Implanted in SCID Mice Using Ex Vivo Gene Therapy

This example illustrates a method for rapidly screening various forms of human cancer to determine susceptibility to treatment by the systemic delivery of anti-angiogenic polypeptides.

The methods for gene transfer, assessment of proviral marking and

20 assessment of transferred gene expression as described in Examples 3 through 9 are repeated using immuno-deficient SCID mice, with the following exceptions. Since SCID mice are more sensitive to  $\gamma$ -irradiation than C57BL6/J mice, the female SCID recipients receive a lower dose of 400cGy of whole body irradiation in contrast to the 950cGy required for C57BL6/J. In

25 addition, since the SCID mice do not possess allelic differences at the CD45 cell surface antigen locus, donor and recipient cells are phenotypically distinguished on the basis of Y chromosome specific sequences using Southern

-27-

blot analysis.

Bone marrow from male donor SCID mice is infected, selected for on the basis of expression of the transferred GFP marker cDNA, and transplanted into irradiated female SCID recipients. Engraftment with provirally marked  
5 cells and expression of the transferred genes is demonstrated. The mice are then separately implanted with a variety of human tumor cell types, e.g., breast adenocarcinoma, lung squamous cell carcinoma, and brain glioblastoma. In each case, the ability of the anti-angiogenic polypeptides to inhibit the growth of the various human tumor cell types is monitored and quantified.

10 Example 11: Evaluating the Efficacy of Retroviral Gene Therapy Vectors Encoding Anti-Angiogenic Polypeptides for Treatment of Ovarian Cancer Using In Vivo Gene Therapy

This example illustrates the feasibility of using retroviral gene therapy vectors encoding anti-angiogenic polypeptides to achieve efficient gene transfer  
15 to established tumors in vivo using a well-established murine model of human ovarian cancer. Following injections, mice are closely monitored for tumor growth and survival.

Eight to ten week old nude mice (Jackson Labs, Bar Harbor are injected intra-peritoneally with  $1 \times 10^7$  PA-1 cells, an ovarian cancer cell-line (ATCC),  
20 and followed until palpable tumors are identified. Viral supernatant for in vivo injection is prepared as follows: Viral producer cells are grown to confluence in DMEM with 10% bovine calf serum, and the medium is then changed. After 24 hours of incubation, the viral conditioned supernatant is filtered through a 0.45  $\mu$ m low protein binding filter, protamine sulfate is added to a final  
25 concentration of 6ug/ml, the solution is aliquoted into 2 ml volumes, and frozen at -80°C. Recipient mice receive three intraperitoneal injections of viral supernatant (2 mls per injection) in addition to the polycation, over a period of

-28-

36 hours. Control mice are injected with medium collected from confluent dishes of NIH3T3 cells. Following injection of the viral conditioned supernatant, the mice are analyzed for survival as well as tumor growth over time as compared to mock injected controls. Results indicate that treatment of the ovarian cancer occurs. At death, the tumors are removed, weighed, and the cells dissociated for DNA extraction for Southern blot analysis to detect recombinant provirus.

Those skilled in the art will be able to ascertain using no more than routine experimentation, many equivalents of the specific embodiments of the invention described herein. These and all other equivalents are intended to be encompassed by the following claims.

In other embodiments, the invention provides methods and compositions for treating diseases and processes that are mediated by angiogenesis including, but not limited to, hemangioma, solid tumors, leukemia, metastasis, telangiectasia, psoriasis, scleroderma, pyogenic granuloma, myocardial angiogenesis, plaque neovascularization, coronary collaterals, cerebral collaterals, arteriovenous malformations, ischemic limb angiogenesis, corneal discases, rubeosis, neovascular glaucoma, diabetic retinopathy, retrolental fibroplasia, arthritis, diabetic neovascularization, macular degeneration, wound healing, peptic ulcer, *Helicobacter* related diseases, fractures, keloids, vasculogenesis, hematopoiesis, ovulation, menstruation, placentation, and cat scratch fever.

What is claimed is:

CLAIMS

1. Use of a nucleic acid molecule which expresses an anti-angiogenic polypeptide selected from the group consisting of human angiostatin, murine angiostatin, human endostatin, murine endostatin, and angiogenesis-inhibiting fragments thereof in the preparation of a medicament for inhibiting tumor growth in a human patient harboring a solid tumor, wherein expression of the anti-angiogenic polypeptide in the patient inhibits angiogenesis in the vicinity of the tumor and/or systemically by diffusion of the recombinant protein to the vascular compartment from secreting transduced cells, thereby inhibiting its growth.

2. Use of a nucleic acid molecule which expresses an anti-angiogenic polypeptide of the formula A-B, wherein

A and B are polypeptide and/or export signal joined by a polypeptide and/or export signal bond;

A contains at least amino acids and comprises kringles 1, 2, and 3 of human or murine angiostatin; and

B contains at least amino acids and includes at least 75% of the amino acid sequence of human or murine endostatin in the preparation of a medicament for inhibiting tumor growth in a human patient harboring a solid tumor, wherein expression of the anti-angiogenic polypeptide in the patient inhibits angiogenesis in the vicinity of the tumor and/or systemically by diffusion of the recombinant protein to the vascular compartment from secreting transduced cells, thereby inhibiting its growth.

3. The use of claim 2, wherein A further comprises kringle region 4 of

-30-

human or murine angiostatin.

4. The use of claim 2 or claim 3, wherein A further comprises kringle 5 of human or murine plasminogen.

5. The use of claim 1 or claim 2, wherein said nucleic acid molecule  
5 constitutes a portion of a viral vector.

6. The use of claim 1 or claim 2, wherein said nucleic acid molecule constitutes a portion of a plasmid.

7. The use of claim 6, wherein said plasmid is carried in a cell-free carrier so that the plasmid transfects living cells of the patient following  
10 plasmid administration, causing expression of the anti-angiogenesis polypeptide and/or export signal in the patient such that angiogenesis in the vicinity of the tumor and/or systemically by diffusion of the recombinant protein to the vascular compartment from secreting transduced cells is inhibited, causing inhibition of tumor growth.

15 8. The use of claim 6, wherein said plasmid has been transfected into animal cells *ex vivo*, wherein said animal cells express the anti-angiogenesis polypeptide to inhibit tumor-associated angiogenesis and tumor growth.

9. The use of claim 5, wherein said viral vector is carried in a cell-free carrier, so that the viral vector is incorporated into living cells of the patient  
20 following viral vector administration, causing expression of the anti-



-31-

angiogenesis polypeptide in the patient such that angiogenesis in the vicinity of the tumor and/or systemically by diffusion of the recombinant protein to the vascular compartment from secreting transduced cells is inhibited, causing inhibition of tumor growth.

5           10. The use of claim 5, wherein animal cells are infected with said viral vector *ex vivo* and then administered to said patient, wherein said animal cells express the anti-angiogenesis polypeptide to inhibit tumor-associated angiogenesis and tumor growth.

11. The use of claim 8, wherein said animal cells are human cells.

10           12. The use of claim 11, wherein said human cells are autologous.

13. The use of claim 11, wherein said human cells are allogeneic.

14. The use of claim 10, wherein said animal cells are human cells.

15. The use of claim 14, wherein said human cells are autologous.

16. The use of claim 14, wherein said human cells are allogeneic.

15           17. The use of claim 5, wherein said viral vector is a retroviral vector.

18. The use of claim 5, wherein said viral vector is a non-retroviral vector selected from the group consisting of adenoviral, adeno-associated, herpes, Simliki Forest virus, and poxvirus vectors.

-32-

19. The use of claim 17, wherein said retroviral vector is Murine Stem Cell Virus or a lentivirus.

20. The use of claim 1, wherein said angiostatin comprises kringles 1, 2 and 3.

5           21. The use of claim 20, wherein said angiostatin further comprises kringle 4.

22. The use of claim 1, wherein said anti-angiogenic polypeptide is a fusion of angiostatin or a biologically active fragment thereof and endostatin or a biologically active fragment thereof.

10           23. The use of claim 1, wherein said nucleic acid molecule includes a nucleotide sequence encoding a signal polypeptide and/or export signal for effecting secretion of said anti-angiogenesis polypeptide.

24. The use of claim 23, wherein said signal polypeptide and/or export signal is plasminogen signal polypeptide and/or export signal.

15           25. The use of claim 1, wherein said nucleic acid molecule includes a nucleotide sequence encoding a preactivation polypeptide and/or export signal for effecting Golgi and/or ER export of the anti-angiogenic polypeptide..

26. The use of claim 25, wherein said preactivation polypeptide and/or export signal is a preactivation polypeptide and/or export signal of a human  
20 protein of the blood coagulation cascade.

27. The use of claim 26, wherein said preactivation polypeptide and/or export signal is human plasminogen preactivation polypeptide and/or export signal.

28. The method of claim 25, wherein the preactivation encoding  
5 sequence is positioned between a signal-encoding sequence and the sequence encoding the anti-angiogenic polypeptide and/or export signal.

29. The use of claim 1, wherein said nucleic acid molecule includes a nucleotide sequence encoding a tag for identification of said anti-angiogenic polypeptide.

10 30. The method of claim 27, wherein said tag is a Flag tag polypeptide and/or export signal.

31. A viral gene therapy vector comprising a nucleic acid molecule which encodes an anti-angiogenic polypeptide selected from the group consisting of human angiostatin, murine angiostatin, human endostatin, murine  
15 endostatin, and angiogenesis-inhibiting fusions and fragments thereof, wherein said viral vector is sufficiently attenuated for use in human gene therapy.

32. A human cell infected with the vector of claim 31.

33. Use of a nucleic acid molecule which expresses in said patient an anti-angiogenic polypeptide selected from the group consisting of human  
20 angiostatin, murine angiostatin, human endostatin, murine endostatin, and angiogenesis-inhibiting fusions and fragments thereof, in the preparation of a

medicament for treating a human patient suffering from diabetic retinopathy, wherein expression of the anti-angiogenic polypeptide in the patient inhibits angiogenesis in the vicinity of the retina.

1/8

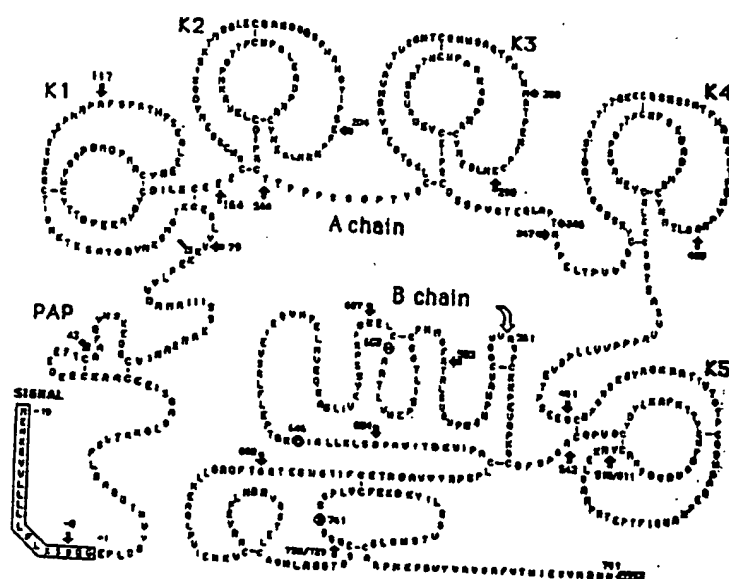


FIG. 1

2/8

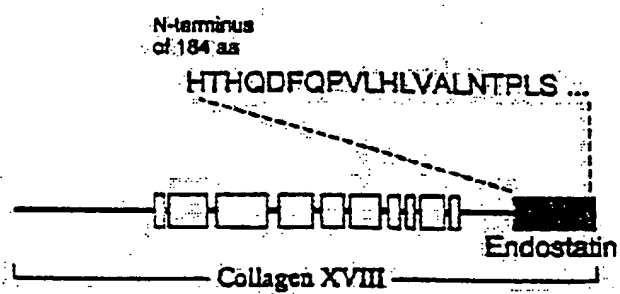


Fig. 2

3/8

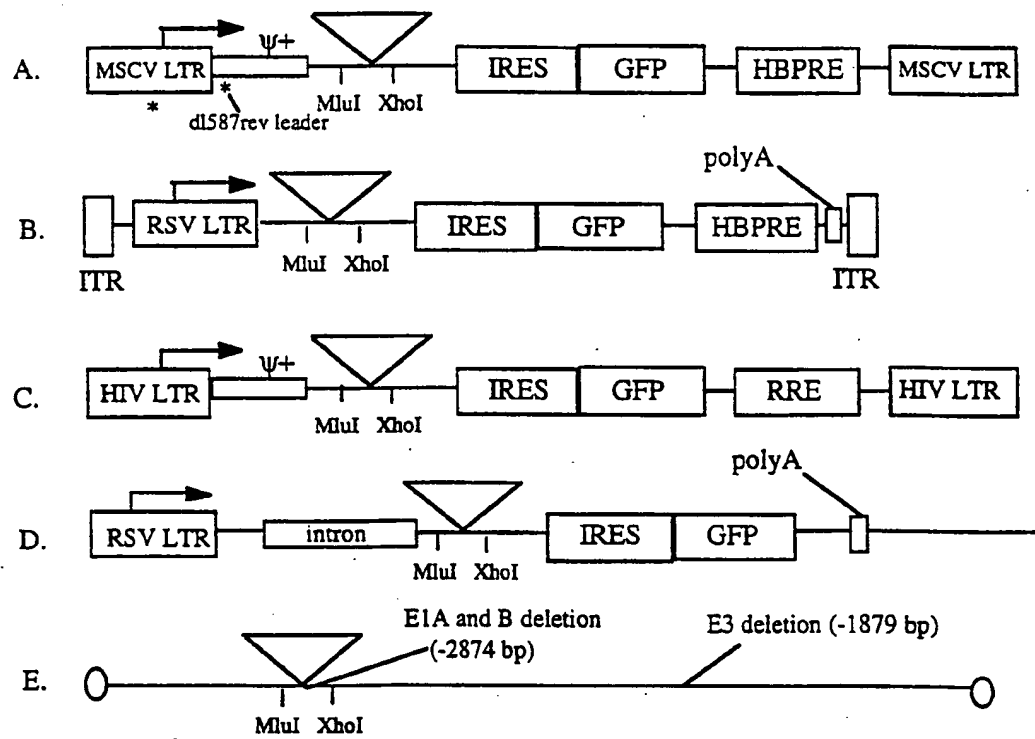


FIG. 3



17:1



FIG. 4



5/8

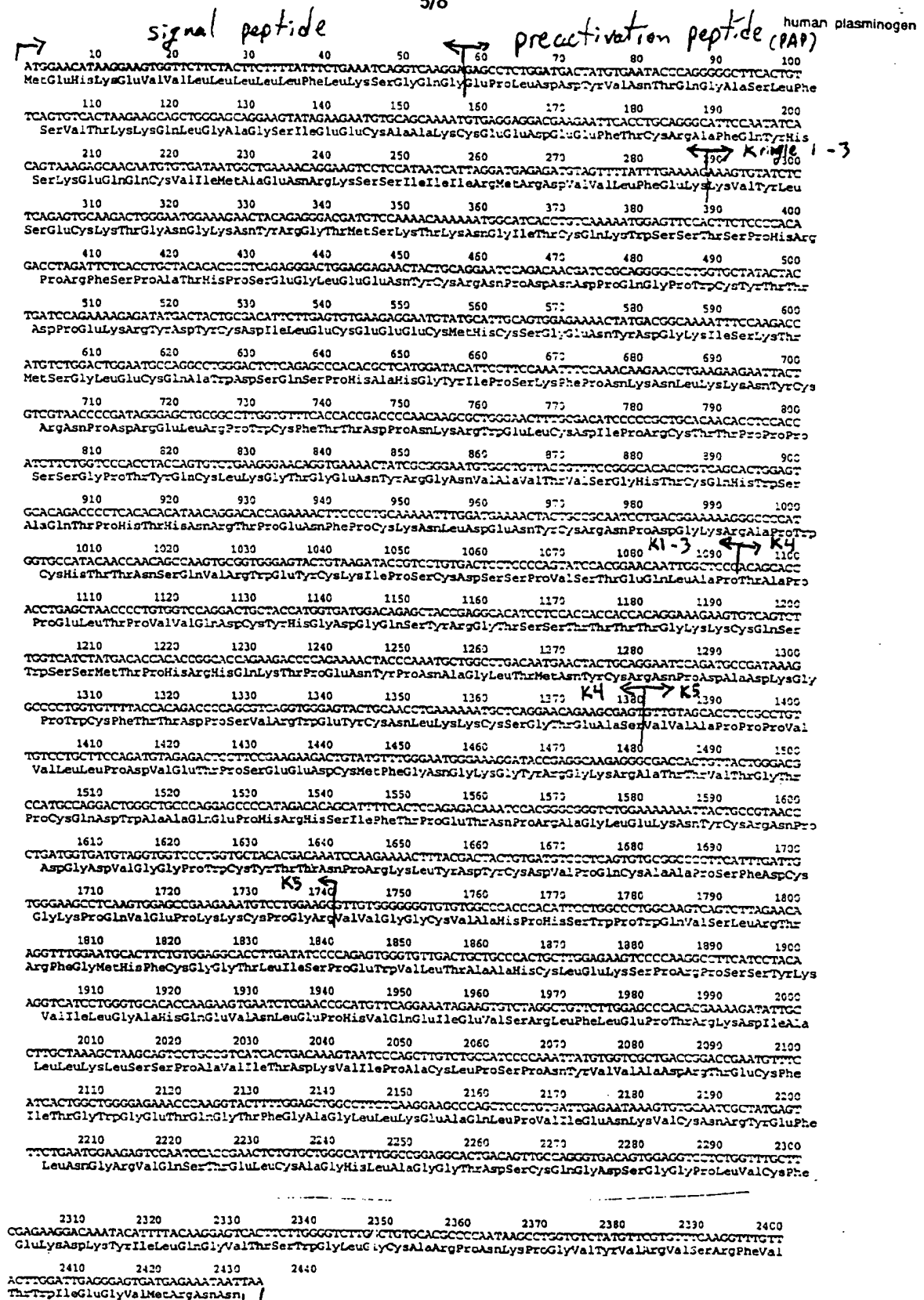


Fig. 5

[illegible]

end mouse endostatin coding sequence

**Fig 6**

Mouse Plasmidogen cDNA

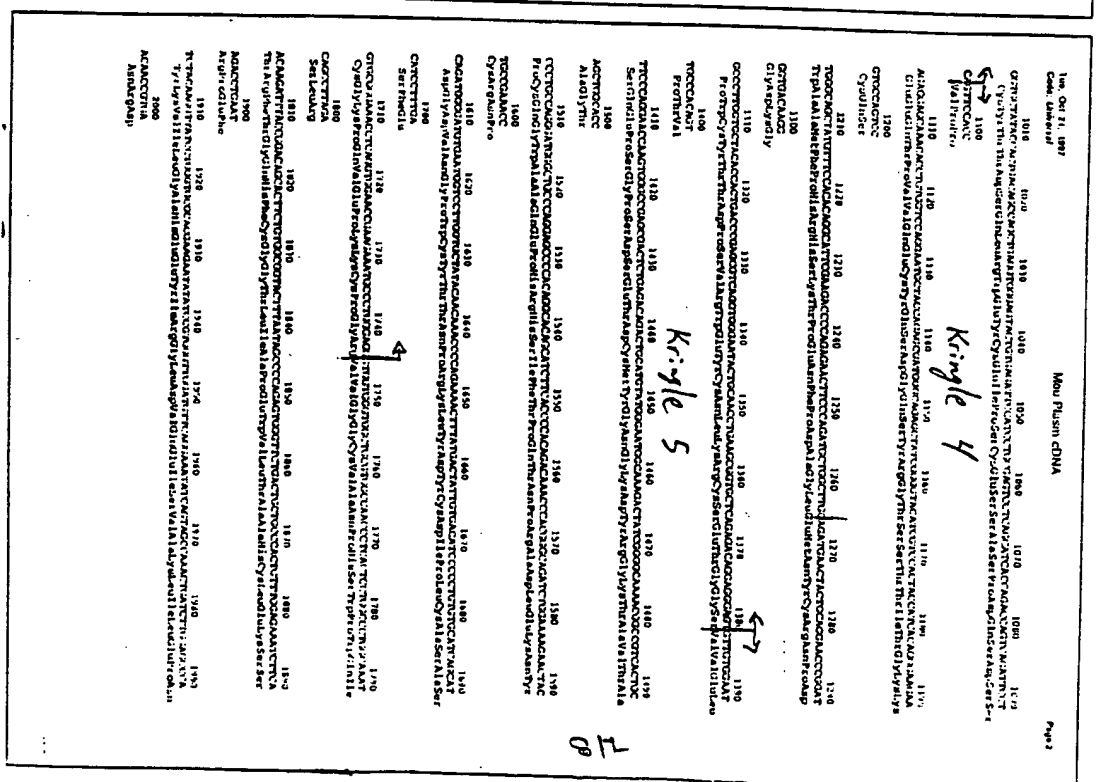
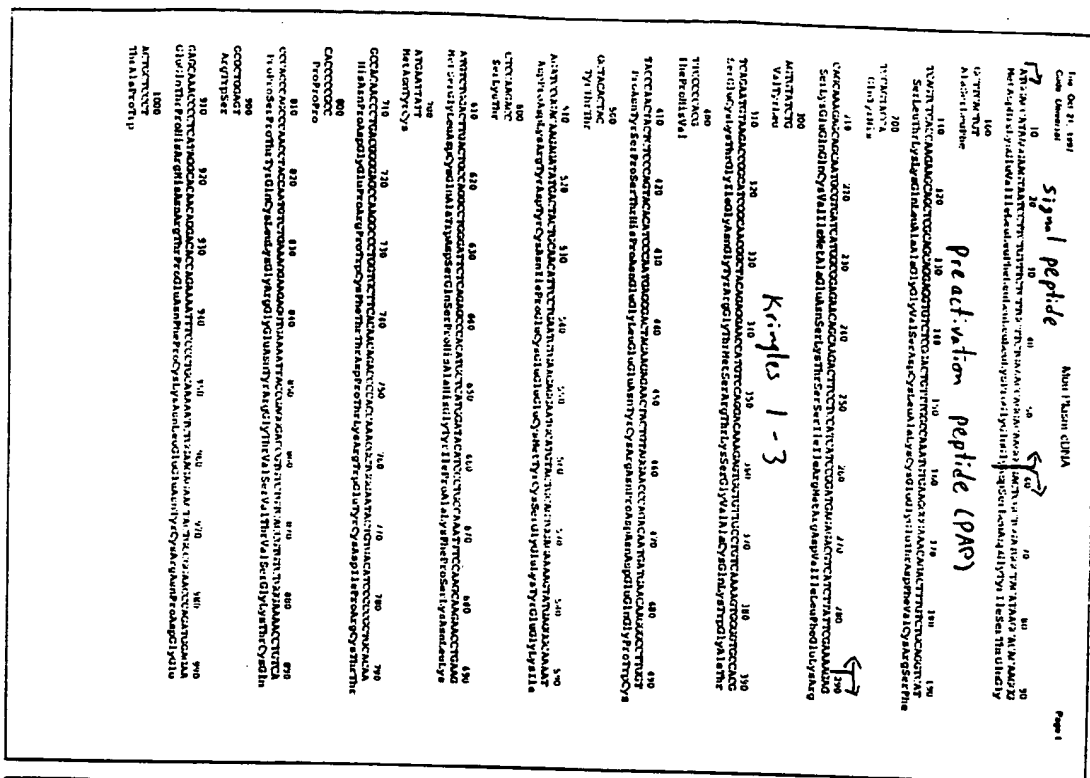


FIG. 7 (Sheet 1 of 2)

Tue, Oct 21, 1997  
Code: Universal

## Mou Plasm cDNA

Page 3

```

2010      2020      2030      2040      2050      2060      2070      2080      2090
CATTGCCCTGCTGAAACTAAGCCGCCAGCCACCATCAGGATAAAGTCATTCCAGCTTGTCTGCCATCTCCAAATTACATGGTTGCTGA
IleAlaLeuLeuLysLeuSerArgProAlaThrIleThrAspLysValIleProAlaCysLeuProSerProAsnTyrMetValAlaAsp

2100
CCCGACAATA
ArgThrIle

2110      2120      2130      2140      2150      2160      2170      2180      2190
TGTACATCACCGGCTGGGAGAGACTCAAGGACTTTCGGTGGCGGTCTCTCAAGGAGGCTCAGCTGCCCTGTGATTGAGAACAAGGTG
CysTyrIleThrGlyTrpGlyGluThrGlnGlyThrPheGlyAlaGlyArgLeuLysGluAlaGlnLeuProValIleGluAsnLysVal

2200
TCCAACCGCG
CysAsnArgVal

2210      2220      2230      2240      2250      2260      2270      2280      2290
TCGAGTATCTGAACAACAGAGTCAAAATCCACGGAGCTCTGTGCCGGCAACTGGCTGGTGGCGTCGACAGCTGCCAAGGCGACAGTGGAG
GluTyrLeuAsnAsnArgValLysSerThrGluLeuCysAlaGlyGlnLeuAlaGlyGlyValAspSerCysGlnGlyAspSerGlyGly

2300
GACCTCTGGT
ProLeuVal

2310      2320      2330      2340      2350      2360      2370      2380      2390
TTGCTTCGAGAAGGACAAGTACATTTTACAAGGAGTCACTTCTTGGGGTCTTGGCTGTGCTCGCCCCAATAAGCCTGGTGTCTACGTTGC
CysPheGluLysAspLysTyrIleLeuGlnGlyValThrSerTrpGlyLeuGlyCysAlaArgProAsnLysProGlyValTyrValArg

2400
TGTCTACCG
ValSerArg

2410      2420      2430      2440      2450      2460      2470      2480      2490
TTTGTGATTGGATTGAAAGGGAGATGAGGAATAACGCTAGGTGGAAGCCGAGCAAACTCTGCTTACTAAAGCTTACTGAATATG
PheValAspTrpIleGluArgGluMetArgAsnAsnEndLeuGlyGlyArgProSerLysThrSerAlaTyrEndSerLeuLeuAsnMet

2500
GGGAGAGGGC
GlyArgGlyLeu

2510      2520      2530      2540      2550      2560      2570      2580      2590
TTAGGGTGTGTTGGAAAACTGACAGTAATCAAACTGGGACACTACACTGAACACAGCTTCCTGTGCCCCCTCAGCCCCCTCCCCCTTTT
ArgValPheGlyLysThrAspSerAsnGlnThrGlyThrLeuHisEndThrThrAlaSerCysArgProSerAlaProProLeuPheLeu

2600
TGTATTATTG
TyrTyrCys

2610      2620      2630      2640      2650      2660      2670      2680      2690
TGGCTAAATTTTCCTGTCTGTGACTTCTGGATTGTTGTGACAAATAGACCATCACTGCTGTGACCTTTGTTGAAAAATAAATCGATACTT
GlyEndAsnPheProValCysGlyLeuLeuAspPheValThrIleAspHisHisCysCysAspLeuCysEndLysEndThrArgTyrLeu

2700
ACTTTG
Leu
```

end plasminogen coding sequence.

## SEQUENCE LISTING

&lt;110&gt; Genetix Pharmaceuticals, Inc.

<120> ANTI-ANGIOGENIC GENE THERAPY VECTORS AND  
THEIR USE IN TREATING ANGIOGENESIS-RELATED DISEASES

&lt;130&gt; 50033/002W01

&lt;140&gt; PCT/US98/xxxxx

&lt;141&gt; 1998-11-20

&lt;150&gt; 08/975,424

&lt;151&gt; 1997-11-20

&lt;160&gt; 20

&lt;170&gt; FastSEQ for Windows Version 3.0

&lt;210&gt; 1

&lt;211&gt; 2433

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(2433)

&lt;400&gt; 1

atg gaa cat aag gaa gtg gtt ctt cta ctt ctt tta ttt ctg aaa tca	48
Met Glu His Lys Glu Val Val Leu Leu Leu Leu Phe Leu Lys Ser	
1 5 10 15	
ggt caa gga gag cct ctg gat gac tat gtg aat acc cag ggg gct tca	96
Gly Gln Gly Glu Pro Leu Asp Asp Tyr Val Asn Thr Gln Gly Ala Ser	
20 25 30	
ctg ttc agt gtc act aag aag cag ctg gga gca gga agt ata gaa gaa	144
Leu Phe Ser Val Thr Lys Lys Gln Leu Gly Ala Gly Ser Ile Glu Glu	
35 40 45	
tgt gca gca aaa tgt gag gag gac gaa gaa ttc acc tgc agg gca ttc	192
Cys Ala Ala Lys Cys Glu Glu Asp Glu Glu Phe Thr Cys Arg Ala Phe	
50 55 60	
caa tat cac agt aaa gag caa caa tgt gtg ata atg gct gaa aac agg	240
Gln Tyr His Ser Lys Glu Gln Gln Cys Val Ile Met Ala Glu Asn Arg	
65 70 75 80	
aag tcc tcc ata atc att agg atg aga gat gta gtt tta ttt gaa aag	288
Lys Ser Ser Ile Ile Ile Arg Met Arg Asp Val Val Leu Phe Glu Lys	
85 90 95	

aaa gtg tat ctc tca gag tgc aag act ggg aat gga aag aac tac aga	336
Lys Val Tyr Leu Ser Glu Cys Lys Thr Gly Asn Gly Lys Asn Tyr Arg	
100 105 110	
ggg acg atg tcc aaa aca aaa aat ggc atc acc tgt caa aaa tgg agt	384
Gly Thr Met Ser Lys Thr Lys Asn Gly Ile Thr Cys Gln Lys Trp Ser	
115 120 125	
tcc act tct ccc cac aga cct aga ttc tca cct gct aca cac ccc tca	432
Ser Thr Ser Pro His Arg Pro Arg Phe Ser Pro Ala Thr His Pro Ser	
130 135 140	
gag gga ctg gag gag aac tac tgc agg aat cca gac aac gat ccg cag	480
Glu Gly Leu Glu Glu Asn Tyr Cys Arg Asn Pro Asp Asn Asp Pro Gln	
145 150 155 160	
ggg ccc tgg tgc tat act act gat cca gaa aag aga tat gac tac tgc	528
Gly Pro Trp Cys Tyr Thr Thr Asp Pro Glu Lys Arg Tyr Asp Tyr Cys	
165 170 175	
gac att ctt gag tgt gaa gag gaa tgt atg cat tgc agt gga gaa aac	576
Asp Ile Leu Glu Cys Glu Glu Glu Cys Met His Cys Ser Gly Glu Asn	
180 185 190	
tat gac ggc aaa att tcc aag acc atg tct gga ctg gaa tgc cag gcc	624
Tyr Asp Gly Lys Ile Ser Lys Thr Met Ser Gly Leu Glu Cys Gln Ala	
195 200 205	
tgg gac tct cag agc cca cac gct cat gga tac att cct tcc aaa ttt	672
Trp Asp Ser Gln Ser Pro His Ala His Gly Tyr Ile Pro Ser Lys Phe	
210 215 220	
cca aac aag aac ctg aag aag aat tac tgt cgt aac ccc gat agg gag	720
Pro Asn Lys Asn Leu Lys Lys Asn Tyr Cys Arg Asn Pro Asp Arg Glu	
225 230 235 240	
ctg cgg cct tgg tgt ttc acc acc gac ccc aac aag cgc tgg gaa ctt	768
Leu Arg Pro Trp Cys Phe Thr Thr Asp Pro Asn Lys Arg Trp Glu Leu	
245 250 255	
tgc gac atc ccc cgc tgc aca aca cct cca cca tct tct ggt ccc acc	816
Cys Asp Ile Pro Arg Cys Thr Thr Pro Pro Pro Ser Ser Gly Pro Thr	
260 265 270	
tac cag tgt ctg aag gga aca ggt gaa aac tat cgc ggg aat gtg gct	864
Tyr Gln Cys Leu Lys Gly Thr Gly Glu Asn Tyr Arg Gly Asn Val Ala	
275 280 285	
gtt acc gtt tcc ggg cac acc tgt cag cac tgg agt gca cag acc cct	912
Val Thr Val Ser Gly His Thr Cys Gln His Trp Ser Ala Gln Thr Pro	
290 295 300	
cac aca cat aac agg aca cca gaa aac ttc ccc tgc aaa aat ttg gat	960
His Thr His Asn Arg Thr Pro Glu Asn Phe Pro Cys Lys Asn Leu Asp	
305 310 315 320	

gaa aac tac tgc cgc aat cct gac gga aaa agg gcc cca tgg tgc cat	1008
Glu Asn Tyr Cys Arg Asn Pro Asp Gly Lys Arg Ala Pro Trp Cys His	
325 330 335	
aca acc aac agc caa gtg cgg tgg gag tac tgt aag ata ccg tcc tgt	1056
Thr Thr Asn Ser Gln Val Arg Trp Glu Tyr Cys Lys Ile Pro Ser Cys	
340 345 350	
gac tcc tcc cca gta tcc acg gaa caa ttg gct ccc aca gca cca cct	1104
Asp Ser Ser Pro Val Ser Thr Glu Gln Leu Ala Pro Thr Ala Pro Pro	
355 360 365	
gag cta acc cct gtg gtc cag gac tgc tac cat ggt gat gga cag agc	1152
Glu Leu Thr Pro Val Val Gln Asp Cys Tyr His Gly Asp Gly Gln Ser	
370 375 380	
tac cga ggc aca tcc tcc acc acc acc aca gga aag aag tgt cag tct	1200
Tyr Arg Gly Thr Ser Ser Thr Thr Thr Thr Thr Gly Lys Lys Cys Gln Ser	
385 390 395 400	
tgg tca tct atg aca cca cac cgg cac cag aag acc cca gaa aac tac	1248
Trp Ser Ser Met Thr Pro His Arg His Gln Lys Thr Pro Glu Asn Tyr	
405 410 415	
cca aat gct ggc ctg aca atg aac tac tgc agg aat cca gat gcc gat	1296
Pro Asn Ala Gly Leu Thr Met Asn Tyr Cys Arg Asn Pro Asp Ala Asp	
420 425 430	
aaa ggc ccc tgg tgt ttt acc aca gac ccc agc gtc agg tgg gag tac	1344
Lys Gly Pro Trp Cys Phe Thr Thr Asp Pro Ser Val Arg Trp Glu Tyr	
435 440 445	
tgc aac ctg aaa aaa tgc tca gga aca gaa gcg agt gtt gta gca cct	1392
Cys Asn Leu Lys Lys Cys Ser Gly Thr Glu Ala Ser Val Val Ala Pro	
450 455 460	
ccg cct gtt gtc ctg ctt cca gat gta gag act cct tcc gaa gaa gac	1440
Pro Pro Val Val Leu Leu Pro Asp Val Glu Thr Pro Ser Glu Glu Asp	
465 470 475 480	
tgt atg ttt ggg aat ggg aaa gga tac cga ggc aag agg gcg acc act	1488
Cys Met Phe Gly Asn Gly Lys Gly Tyr Arg Gly Lys Arg Ala Thr Thr	
485 490 495	
gtt act ggg acg cca tgc cag gac tgg gct gcc cag gag ccc cat aga	1536
Val Thr Gly Thr Pro Cys Gln Asp Trp Ala Ala Gln Glu Pro His Arg	
500 505 510	
cac agc att ttc act cca gag aca aat cca cgg gcg ggt ctg gaa aaa	1584
His Ser Ile Phe Thr Pro Glu Thr Asn Pro Arg Ala Gly Leu Glu Lys	
515 520 525	
aat tac tgc cgt aac cct gat ggt gat gta ggt ggt ccc tgg tgc tac	1632
Asn Tyr Cys Arg Asn Pro Asp Gly Asp Val Gly Gly Pro Trp Cys Tyr	

530	535	540	
acg aca aat cca aga aaa ctt tac gac tac tgt gat gtc cct cag tgt			1680
Thr Thr Asn Pro Arg Lys Leu Tyr Asp Tyr Cys Asp Val Pro Gln Cys			
545	550	555	560
gcg gcc cct tca ttt gat tgt ggg aag cct caa gtg gag ccg aag aaa			1728
Ala Ala Pro Ser Phe Asp Cys Gly Lys Pro Gln Val Glu Pro Lys Lys			
	565	570	575
tgt cct gga agg gtt gtg ggg ggg tgt gtg gcc cac cca cat tcc tgg			1776
Cys Pro Gly Arg Val Val Gly Gly Cys Val Ala His Pro His Ser Trp			
	580	585	590
ccc tgg caa gtc agt ctt aga aca agg ttt gga atg cac ttc tgt gga			1824
Pro Trp Gln Val Ser Leu Arg Thr Arg Phe Gly Met His Phe Cys Gly			
	595	600	605
ggc acc ttg ata tcc cca gag tgg gtg ttg act gct gcc cac tgc ttg			1872
Gly Thr Leu Ile Ser Pro Glu Trp Val Leu Thr Ala Ala His Cys Leu			
	610	615	620
gag aag tcc cca agg cct tca tcc tac aag gtc atc ctg ggt gca cac			1920
Glu Lys Ser Pro Arg Pro Ser Ser Tyr Lys Val Ile Leu Gly Ala His			
	625	630	635
caa gaa gtg aat ctc gaa ccg cat gtt cag gaa ata gaa gtg tct agg			1968
Gln Glu Val Asn Leu Glu Pro His Val Gln Glu Ile Glu Val Ser Arg			
	645	650	655
ctg ttc ttg gag ccc aca cga aaa gat att gcc ttg cta aag cta agc			2016
Leu Phe Leu Glu Pro Thr Arg Lys Asp Ile Ala Leu Leu Lys Leu Ser			
	660	665	670
agt cct gcc gtc atc act gac aaa gta atc cca gct tgt ctg cca tcc			2064
Ser Pro Ala Val Ile Thr Asp Lys Val Ile Pro Ala Cys Leu Pro Ser			
	675	680	685
cca aat tat gtg gtc gct gac cgg acc gaa tgt ttc atc act ggc tgg			2112
Pro Asn Tyr Val Val Ala Asp Arg Thr Glu Cys Phe Ile Thr Gly Trp			
	690	695	700
gga gaa acc caa ggt act ttt gga gct ggc ctt ctc aag gaa gcc cag			2160
Gly Glu Thr Gln Gly Thr Phe Gly Ala Gly Leu Leu Lys Glu Ala Gln			
	705	710	715
ctc cct gtg att gag aat aaa gtg tgc aat cgc tat gag ttt ctg aat			2208
Leu Pro Val Ile Glu Asn Lys Val Cys Asn Arg Tyr Glu Phe Leu Asn			
	725	730	735
gga aga gtc caa tcc acc gaa ctc tgt gct ggg cat ttg gcc gga ggc			2256
Gly Arg Val Gln Ser Thr Glu Leu Cys Ala Gly His Leu Ala Gly Gly			
	740	745	750
act gac agt tgc cag ggt gac agt gga ggt cct ctg gtt tgc ttc gag			2304



```

Thr Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Phe Glu
    755                                760                                765

aag gac aaa tac att tta caa gga gtc act tct tgg ggt ctt ggc tgt      2352
Lys Asp Lys Tyr Ile Leu Gln Gly Val Thr Ser Trp Gly Leu Gly Cys
    770                                775                                780

gca cgc ccc aat aag cct ggt gtc tat gtt cgt gtt tca agg ttt gtt      2400
Ala Arg Pro Asn Lys Pro Gly Val Tyr Val Arg Val Ser Arg Phe Val
    785                                790                                795                                800

act tgg att gag gga gtg atg aga aat aat taa      2433
Thr Trp Ile Glu Gly Val Met Arg Asn Asn *
    805                                810

```

```

<210> 2
<211> 810
<212> PRT
<213> Homo sapiens

```

```

<400> 2
Met Glu His Lys Glu Val Val Leu Leu Leu Leu Phe Leu Lys Ser
  1                                5                                10                                15
Gly Gln Gly Glu Pro Leu Asp Asp Tyr Val Asn Thr Gln Gly Ala Ser
    20                                25                                30
Leu Phe Ser Val Thr Lys Lys Gln Leu Gly Ala Gly Ser Ile Glu Glu
    35                                40                                45
Cys Ala Ala Lys Cys Glu Glu Asp Glu Glu Phe Thr Cys Arg Ala Phe
    50                                55                                60
Gln Tyr His Ser Lys Glu Gln Gln Cys Val Ile Met Ala Glu Asn Arg
    65                                70                                75                                80
Lys Ser Ser Ile Ile Ile Arg Met Arg Asp Val Val Leu Phe Glu Lys
    85                                90                                95
Lys Val Tyr Leu Ser Glu Cys Lys Thr Gly Asn Gly Lys Asn Tyr Arg
    100                                105                                110
Gly Thr Met Ser Lys Thr Lys Asn Gly Ile Thr Cys Gln Lys Trp Ser
    115                                120                                125
Ser Thr Ser Pro His Arg Pro Arg Phe Ser Pro Ala Thr His Pro Ser
    130                                135                                140
Glu Gly Leu Glu Glu Asn Tyr Cys Arg Asn Pro Asp Asn Asp Pro Gln
    145                                150                                155                                160
Gly Pro Trp Cys Tyr Thr Thr Asp Pro Glu Lys Arg Tyr Asp Tyr Cys
    165                                170                                175
Asp Ile Leu Glu Cys Glu Glu Glu Cys Met His Cys Ser Gly Glu Asn
    180                                185                                190
Tyr Asp Gly Lys Ile Ser Lys Thr Met Ser Gly Leu Glu Cys Gln Ala
    195                                200                                205
Trp Asp Ser Gln Ser Pro His Ala His Gly Tyr Ile Pro Ser Lys Phe
    210                                215                                220
Pro Asn Lys Asn Leu Lys Lys Asn Tyr Cys Arg Asn Pro Asp Arg Glu
    225                                230                                235                                240
Leu Arg Pro Trp Cys Phe Thr Thr Asp Pro Asn Lys Arg Trp Glu Leu
    245                                250                                255
Cys Asp Ile Pro Arg Cys Thr Thr Pro Pro Pro Ser Ser Gly Pro Thr

```

6

Gly Glu Thr Gln Gly Thr Phe Gly Ala Gly Leu Leu Lys Glu Ala Gln  
 705 710 715 720  
 Leu Pro Val Ile Glu Asn Lys Val Cys Asn Arg Tyr Glu Phe Leu Asn  
 725 730 735  
 Gly Arg Val Gln Ser Thr Glu Leu Cys Ala Gly His Leu Ala Gly Gly  
 740 745 750  
 Thr Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Phe Glu  
 755 760 765  
 Lys Asp Lys Tyr Ile Leu Gln Gly Val Thr Ser Trp Gly Leu Gly Cys  
 770 775 780  
 Ala Arg Pro Asn Lys Pro Gly Val Tyr Val Arg Val Ser Arg Phe Val  
 785 790 795 800  
 Thr Trp Ile Glu Gly Val Met Arg Asn Asn  
 805 810

&lt;210&gt; 3

&lt;211&gt; 2696

&lt;212&gt; DNA

&lt;213&gt; Mus musculus

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(2436)

&lt;400&gt; 3

atg gac cat aag gaa gta atc ctt ctg ttt ctc ttg ctt ctg aaa cca 48  
 Met Asp His Lys Glu Val Ile Leu Leu Phe Leu Leu Leu Leu Lys Pro  
 1 5 10 15

gga caa ggg gac tcg ctg gat ggc tac ata agc aca caa ggg gct tca 96  
 Gly Gln Gly Asp Ser Leu Asp Gly Tyr Ile Ser Thr Gln Gly Ala Ser  
 20 25 30

ctg ttc agt ctc acc aag aag cag ctc gca gca gga ggt gtc tcg gac 144  
 Leu Phe Ser Leu Thr Lys Lys Gln Leu Ala Ala Gly Gly Val Ser Asp  
 35 40 45

tgt ttg gcc aaa tgt gaa ggg gaa aca gac ttt gtc tgc agg tca ttc 192  
 Cys Leu Ala Lys Cys Glu Gly Glu Thr Asp Phe Val Cys Arg Ser Phe  
 50 55 60

cag tac cac agc aaa gag cag caa tgc gtg atc atg gcg gag aac agc 240  
 Gln Tyr His Ser Lys Glu Gln Gln Cys Val Ile Met Ala Glu Asn Ser  
 65 70 75 80

aag act tcc tcc atc atc cgg atg aga gac gtc atc tta ttc gaa aag 288  
 Lys Thr Ser Ser Ile Ile Arg Met Arg Asp Val Ile Leu Phe Glu Lys  
 85 90 95

aga gtg tat ctg tca gaa tgt aag acc ggc atc ggc aac ggc tac aga 336  
 Arg Val Tyr Leu Ser Glu Cys Lys Thr Gly Ile Gly Asn Gly Tyr Arg  
 100 105 110

gga acc atg tcc agg aca aag agt ggt gtt gcc tgt caa aag tgg ggt 384  
 Gly Thr Met Ser Arg Thr Lys Ser Gly Val Ala Cys Gln Lys Trp Gly

115	120	125	
gcc acg ttc ccc cac gta ccc aac tac tct ccc agt aca cat ccc aat Ala Thr Phe Pro His Val Pro Asn Tyr Ser Pro Ser Thr His Pro Asn 130 135 140			432
gag gga cta gaa gag aac tac tgt agg aac cca gac aat gat gaa caa Glu Gly Leu Glu Glu Asn Tyr Cys Arg Asn Pro Asp Asn Asp Glu Gln 145 150 155 160			480
ggg cct tgg tgc tac act aca gat ccg gac aag aga tat gac tac tgc Gly Pro Trp Cys Tyr Thr Thr Asp Pro Asp Lys Arg Tyr Asp Tyr Cys 165 170 175			528
aac att cct gaa tgt gaa gag gaa tgc atg tac tgc agt gga gaa aag Asn Ile Pro Glu Cys Glu Glu Glu Cys Met Tyr Cys Ser Gly Glu Lys 180 185 190			576
tat gag ggc aaa atc tcc aag acc atg tct gga ctt gac tgc cag gcc Tyr Glu Gly Lys Ile Ser Lys Thr Met Ser Gly Leu Asp Cys Gln Ala 195 200 205			624
tgg gat tct cag agc cca cat gct cat gga tac atc cct gcc aaa ttt Trp Asp Ser Gln Ser Pro His Ala His Gly Tyr Ile Pro Ala Lys Phe 210 215 220			672
cca agc aag aac ctg aag atg aat tat tgc cac aac cct gac ggg gag Pro Ser Lys Asn Leu Lys Met Asn Tyr Cys His Asn Pro Asp Gly Glu 225 230 235 240			720
cca agg ccc tgg tgc ttc aca aca gac ccc acc aaa cgc tgg gaa tac Pro Arg Pro Trp Cys Phe Thr Thr Asp Pro Thr Lys Arg Trp Glu Tyr 245 250 255			768
tgt gac atc ccc cgc tgc aca aca ccc ccg ccc cca ccc agc cca acc Cys Asp Ile Pro Arg Cys Thr Thr Pro Pro Pro Pro Pro Ser Pro Thr 260 265 270			816
tac caa tgt ctg aaa gga aga ggt gaa aat tac cga ggg acc gtg tct Tyr Gln Cys Leu Lys Gly Arg Gly Glu Asn Tyr Arg Gly Thr Val Ser 275 280 285			864
gtc acc gtg tct ggg aaa acc tgt cag cgc tgg agt gag caa acc cct Val Thr Val Ser Gly Lys Thr Cys Gln Arg Trp Ser Glu Gln Thr Pro 290 295 300			912
cat agg cac aac agg aca cca gaa aat ttc ccc tgc aaa aat ctg gaa His Arg His Asn Arg Thr Pro Glu Asn Phe Pro Cys Lys Asn Leu Glu 305 310 315 320			960
gag aac tac tgc cgg aac cca gat gga gaa act gct ccc tgg tgc tat Glu Asn Tyr Cys Arg Asn Pro Asp Gly Glu Thr Ala Pro Trp Cys Tyr 325 330 335			1008
acc act gac agc cag ctg agg tgg gag tac tgt gag att cca tcc tgc			1056

Thr Thr Asp Ser Gln Leu Arg Trp Glu Tyr Cys Glu Ile Pro Ser Cys	
340 345 350	
gag tcc tca gca tca cca gac cag tca gat tcc tca gtt cca cca gag	1104
Glu Ser Ser Ala Ser Pro Asp Gln Ser Asp Ser Ser Val Pro Pro Glu	
355 360 365	
gag caa aca cct gtg gtc cag gaa tgc tac cag agc gat ggg cag agc	1152
Glu Gln Thr Pro Val Val Gln Glu Cys Tyr Gln Ser Asp Gly Gln Ser	
370 375 380	
tat cgg ggt aca tcg tcc act acc atc aca ggg aag aag tgc cag tcc	1200
Tyr Arg Gly Thr Ser Ser Thr Thr Ile Thr Gly Lys Lys Cys Gln Ser	
385 390 395 400	
tgg gca gct atg ttt cca cac agg cat tcg aag acc cca gag aac ttc	1248
Trp Ala Ala Met Phe Pro His Arg His Ser Lys Thr Pro Glu Asn Phe	
405 410 415	
cca gat gct ggc ttg gag atg aac tac tgc agg aac ccg gat ggt gac	1296
Pro Asp Ala Gly Leu Glu Met Asn Tyr Cys Arg Asn Pro Asp Gly Asp	
420 425 430	
aag ggc cct tgg tgc tac acc act gac ccg agc gtc agg tgg gaa tac	1344
Lys Gly Pro Trp Cys Tyr Thr Thr Asp Pro Ser Val Arg Trp Glu Tyr	
435 440 445	
tgc aac ctg aag cgg tgc tca gag aca gga ggg agt gtt gtg gaa ttg	1392
Cys Asn Leu Lys Arg Cys Ser Glu Thr Gly Gly Ser Val Val Glu Leu	
450 455 460	
ccc aca gtt tcc cag gaa cca agt ggg ccg agc gac tct gag aca gac	1440
Pro Thr Val Ser Gln Glu Pro Ser Gly Pro Ser Asp Ser Glu Thr Asp	
465 470 475 480	
tgc atg tat ggg aat ggc aaa gac tat cgg ggc aaa acg gcc gtc act	1488
Cys Met Tyr Gly Asn Gly Lys Asp Tyr Arg Gly Lys Thr Ala Val Thr	
485 490 495	
gca gct ggc acc ccc tgc cag gga tgg gct gcc cag gag ccc cac agg	1536
Ala Ala Gly Thr Pro Cys Gln Gly Trp Ala Ala Gln Glu Pro His Arg	
500 505 510	
cac agc atc ttc acc cca cag aca aac cca ccg gca gat ctg gaa aag	1584
His Ser Ile Phe Thr Pro Gln Thr Asn Pro Arg Ala Asp Leu Glu Lys	
515 520 525	
aac tac tgc cga aac cca gat ggg gat gtg aat ggt cct tgg tgc tat	1632
Asn Tyr Cys Arg Asn Pro Asp Gly Asp Val Asn Gly Pro Trp Cys Tyr	
530 535 540	
aca aca aac ccc aga aaa ctt tat gac tat tgt gac atc ccc ctg tgt	1680
Thr Thr Asn Pro Arg Lys Leu Tyr Asp Tyr Cys Asp Ile Pro Leu Cys	
545 550 555 560	

gca tca gca tca tcc ttt gag tgc ggg aaa cct cag gtg gaa ccg aag	1728
Ala Ser Ala Ser Ser Phe Glu Cys Gly Lys Pro Gln Val Glu Pro Lys	
565 570 575	
aaa tgc cct ggg agg gtg gtg ggt ggc tgc gtg gcc aac cct cac tcc	1776
Lys Cys Pro Gly Arg Val Val Gly Gly Cys Val Ala Asn Pro His Ser	
580 585 590	
tgg ccc tgg caa atc agc ctt aga aca aga ttt acc gga cag cac ttc	1824
Trp Pro Trp Gln Ile Ser Leu Arg Thr Arg Phe Thr Gly Gln His Phe	
595 600 605	
tgt ggc ggt act tta ata gcc cca gag tgg gtt ctg act gct gcc cac	1872
Cys Gly Gly Thr Leu Ile Ala Pro Glu Trp Val Leu Thr Ala Ala His	
610 615 620	
tgt ttg gag aaa tct tca aga cct gaa ttc tac aag gtt atc ctg ggt	1920
Cys Leu Glu Lys Ser Ser Arg Pro Glu Phe Tyr Lys Val Ile Leu Gly	
625 630 635 640	
gcg cac gaa gaa tat atc cgt ggg ttg gat gtt cag gaa ata tca gta	1968
Ala His Glu Glu Tyr Ile Arg Gly Leu Asp Val Gln Glu Ile Ser Val	
645 650 655	
gcc aaa ctg atc ttg gag ccc aac aac cgt gac att gcc ctg ctg aaa	2016
Ala Lys Leu Ile Leu Glu Pro Asn Asn Arg Asp Ile Ala Leu Leu Lys	
660 665 670	
cta agc cgc cca gcc acc atc acg gat aaa gtc att cca gct tgt ctg	2064
Leu Ser Arg Pro Ala Thr Ile Thr Asp Lys Val Ile Pro Ala Cys Leu	
675 680 685	
cca tct cca aat tac atg gtt gct gac cgg aca ata tgt tac atc acc	2112
Pro Ser Pro Asn Tyr Met Val Ala Asp Arg Thr Ile Cys Tyr Ile Thr	
690 695 700	
ggc tgg gga gag act caa ggg act ttc ggt gcc ggt cgt ctc aag gag	2160
Gly Trp Gly Glu Thr Gln Gly Thr Phe Gly Ala Gly Arg Leu Lys Glu	
705 710 715 720	
gct cag ctg cct gtg att gag aac aag gtg tgc aac cgc gtc gag tat	2208
Ala Gln Leu Pro Val Ile Glu Asn Lys Val Cys Asn Arg Val Glu Tyr	
725 730 735	
ctg aac aac aga gtc aaa tcc acg gag ctc tgt gcc ggg caa ctg gct	2256
Leu Asn Asn Arg Val Lys Ser Thr Glu Leu Cys Ala Gly Gln Leu Ala	
740 745 750	
ggc ggc gtc gac agc tgc caa ggc gac agt gga gga cct ctg gtt tgc	2304
Gly Gly Val Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys	
755 760 765	
ttc gag aag gac aag tac att tta caa gga gtc act tct tgg ggt ctt	2352
Phe Glu Lys Asp Lys Tyr Ile Leu Gln Gly Val Thr Ser Trp Gly Leu	
770 775 780	

ggc tgt gct cgc ccc aat aag cct ggt gtc tac gtt cgt gtc tca cgg 2400  
 Gly Cys Ala Arg Pro Asn Lys Pro Gly Val Tyr Val Arg Val Ser Arg  
 785 790 795 800

ttt gtt gat tgg att gaa agg gag atg agg aat aac tgactaggtg 2446  
 Phe Val Asp Trp Ile Glu Arg Glu Met Arg Asn Asn  
 805 810

gaaggccgag caaaacctct gcttactaaa gcttactgaa tatggggaga gggcttaggg 2506  
 tgtttgaaaa aactgacagt aatcaaactg ggacactaca ctgaaccaca gcttctgtgc 2566  
 gccccacagc cccctccctt tttttgtatt attgtgggta aaattttcct gtctgtggac 2626  
 ttctggattt tgtgacaata gaccatcact gctgtgacct ttgttgaaaa taaactcgat 2686  
 acttactttg 2696

<210> 4  
 <211> 812  
 <212> PRT  
 <213> Mus musculus

<400> 4  
 Met Asp His Lys Glu Val Ile Leu Leu Phe Leu Leu Leu Leu Lys Pro  
 1 5 10 15  
 Gly Gln Gly Asp Ser Leu Asp Gly Tyr Ile Ser Thr Gln Gly Ala Ser  
 20 25 30  
 Leu Phe Ser Leu Thr Lys Lys Gln Leu Ala Ala Gly Gly Val Ser Asp  
 35 40 45  
 Cys Leu Ala Lys Cys Glu Gly Glu Thr Asp Phe Val Cys Arg Ser Phe  
 50 55 60  
 Gln Tyr His Ser Lys Glu Gln Gln Cys Val Ile Met Ala Glu Asn Ser  
 65 70 75 80  
 Lys Thr Ser Ser Ile Ile Arg Met Arg Asp Val Ile Leu Phe Glu Lys  
 85 90 95  
 Arg Val Tyr Leu Ser Glu Cys Lys Thr Gly Ile Gly Asn Gly Tyr Arg  
 100 105 110  
 Gly Thr Met Ser Arg Thr Lys Ser Gly Val Ala Cys Gln Lys Trp Gly  
 115 120 125  
 Ala Thr Phe Pro His Val Pro Asn Tyr Ser Pro Ser Thr His Pro Asn  
 130 135 140  
 Glu Gly Leu Glu Glu Asn Tyr Cys Arg Asn Pro Asp Asn Asp Glu Gln  
 145 150 155 160  
 Gly Pro Trp Cys Tyr Thr Thr Asp Pro Asp Lys Arg Tyr Asp Tyr Cys  
 165 170 175  
 Asn Ile Pro Glu Cys Glu Glu Glu Cys Met Tyr Cys Ser Gly Glu Lys  
 180 185 190  
 Tyr Glu Gly Lys Ile Ser Lys Thr Met Ser Gly Leu Asp Cys Gln Ala  
 195 200 205  
 Trp Asp Ser Gln Ser Pro His Ala His Gly Tyr Ile Pro Ala Lys Phe  
 210 215 220  
 Pro Ser Lys Asn Leu Lys Met Asn Tyr Cys His Asn Pro Asp Gly Glu  
 225 230 235 240  
 Pro Arg Pro Trp Cys Phe Thr Thr Asp Pro Thr Lys Arg Trp Glu Tyr  
 245 250 255  
 Cys Asp Ile Pro Arg Cys Thr Thr Pro Pro Pro Pro Ser Pro Thr  
 260 265 270

Tyr Gln Cys Leu Lys Gly Arg Gly Glu Asn Tyr Arg Gly Thr Val Ser  
 275 280 285  
 Val Thr Val Ser Gly Lys Thr Cys Gln Arg Trp Ser Glu Gln Thr Pro  
 290 295 300  
 His Arg His Asn Arg Thr Pro Glu Asn Phe Pro Cys Lys Asn Leu Glu  
 305 310 315 320  
 Glu Asn Tyr Cys Arg Asn Pro Asp Gly Glu Thr Ala Pro Trp Cys Tyr  
 325 330 335  
 Thr Thr Asp Ser Gln Leu Arg Trp Glu Tyr Cys Glu Ile Pro Ser Cys  
 340 345 350  
 Glu Ser Ser Ala Ser Pro Asp Gln Ser Asp Ser Ser Val Pro Pro Glu  
 355 360 365  
 Glu Gln Thr Pro Val Val Gln Glu Cys Tyr Gln Ser Asp Gly Gln Ser  
 370 375 380  
 Tyr Arg Gly Thr Ser Ser Thr Thr Ile Thr Gly Lys Lys Cys Gln Ser  
 385 390 395 400  
 Trp Ala Ala Met Phe Pro His Arg His Ser Lys Thr Pro Glu Asn Phe  
 405 410 415  
 Pro Asp Ala Gly Leu Glu Met Asn Tyr Cys Arg Asn Pro Asp Gly Asp  
 420 425 430  
 Lys Gly Pro Trp Cys Tyr Thr Thr Asp Pro Ser Val Arg Trp Glu Tyr  
 435 440 445  
 Cys Asn Leu Lys Arg Cys Ser Glu Thr Gly Gly Ser Val Val Glu Leu  
 450 455 460  
 Pro Thr Val Ser Gln Glu Pro Ser Gly Pro Ser Asp Ser Glu Thr Asp  
 465 470 475 480  
 Cys Met Tyr Gly Asn Gly Lys Asp Tyr Arg Gly Lys Thr Ala Val Thr  
 485 490 495  
 Ala Ala Gly Thr Pro Cys Gln Gly Trp Ala Ala Gln Glu Pro His Arg  
 500 505 510  
 His Ser Ile Phe Thr Pro Gln Thr Asn Pro Arg Ala Asp Leu Glu Lys  
 515 520 525  
 Asn Tyr Cys Arg Asn Pro Asp Gly Asp Val Asn Gly Pro Trp Cys Tyr  
 530 535 540  
 Thr Thr Asn Pro Arg Lys Leu Tyr Asp Tyr Cys Asp Ile Pro Leu Cys  
 545 550 555 560  
 Ala Ser Ala Ser Ser Phe Glu Cys Gly Lys Pro Gln Val Glu Pro Lys  
 565 570 575  
 Lys Cys Pro Gly Arg Val Val Gly Gly Cys Val Ala Asn Pro His Ser  
 580 585 590  
 Trp Pro Trp Gln Ile Ser Leu Arg Thr Arg Phe Thr Gly Gln His Phe  
 595 600 605  
 Cys Gly Gly Thr Leu Ile Ala Pro Glu Trp Val Leu Thr Ala Ala His  
 610 615 620  
 Cys Leu Glu Lys Ser Ser Arg Pro Glu Phe Tyr Lys Val Ile Leu Gly  
 625 630 635 640  
 Ala His Glu Glu Tyr Ile Arg Gly Leu Asp Val Gln Glu Ile Ser Val  
 645 650 655  
 Ala Lys Leu Ile Leu Glu Pro Asn Asn Arg Asp Ile Ala Leu Leu Lys  
 660 665 670  
 Leu Ser Arg Pro Ala Thr Ile Thr Asp Lys Val Ile Pro Ala Cys Leu  
 675 680 685  
 Pro Ser Pro Asn Tyr Met Val Ala Asp Arg Thr Ile Cys Tyr Ile Thr  
 690 695 700  
 Gly Trp Gly Glu Thr Gln Gly Thr Phe Gly Ala Gly Arg Leu Lys Glu



```

705              710              715              720
Ala Gln Leu Pro Val Ile Glu Asn Lys Val Cys Asn Arg Val Glu Tyr
              725              730              735
Leu Asn Asn Arg Val Lys Ser Thr Glu Leu Cys Ala Gly Gln Leu Ala
              740              745              750
Gly Gly Val Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys
              755              760              765
Phe Glu Lys Asp Lys Tyr Ile Leu Gln Gly Val Thr Ser Trp Gly Leu
              770              775              780
Gly Cys Ala Arg Pro Asn Lys Pro Gly Val Tyr Val Arg Val Ser Arg
785              790              795              800
Phe Val Asp Trp Ile Glu Arg Glu Met Arg Asn Asn
              805              810

```

```

<210> 5
<211> 1083
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> (1)...(1083)

```

```

<400> 5
tat ctc tca gag tgc aag act ggg aat gga aag aac tac aga ggg acg      48
Tyr Leu Ser Glu Cys Lys Thr Gly Asn Gly Lys Asn Tyr Arg Gly Thr
  1              5              10              15

atg tcc aaa aca aaa aat ggc atc acc tgt caa aaa tgg agt tcc act      96
Met Ser Lys Thr Lys Asn Gly Ile Thr Cys Gln Lys Trp Ser Ser Thr
              20              25              30

tct ccc cac aga cct aga ttc tca cct gct aca cac ccc tca gag gga      144
Ser Pro His Arg Pro Arg Phe Ser Pro Ala Thr His Pro Ser Glu Gly
              35              40              45

ctg gag gag aac tac tgc agg aat cca gac aac gat ccg cag ggg ccc      192
Leu Glu Glu Asn Tyr Cys Arg Asn Pro Asp Asn Asp Pro Gln Gly Pro
              50              55              60

tgg tgc tat act act gat cca gaa aag aga tat gac tac tgc gac att      240
Trp Cys Tyr Thr Thr Asp Pro Glu Lys Arg Tyr Asp Tyr Cys Asp Ile
              65              70              75              80

ctt gag tgt gaa gag gaa tgt atg cat tgc agt gga gaa aac tat gac      288
Leu Glu Cys Glu Glu Glu Cys Met His Cys Ser Gly Glu Asn Tyr Asp
              85              90              95

ggc aaa att tcc aag acc atg tct gga ctg gaa tgc cag gcc tgg gac      336
Gly Lys Ile Ser Lys Thr Met Ser Gly Leu Glu Cys Gln Ala Trp Asp
              100              105              110

tct cag agc cca cac gct cat gga tac att cct tcc aaa ttt cca aac      384
Ser Gln Ser Pro His Ala His Gly Tyr Ile Pro Ser Lys Phe Pro Asn
              115              120              125

```

aag aac ctg aag aag aat tac tgt cgt aac ccc gat agg gag ctg cgg	432
Lys Asn Leu Lys Lys Asn Tyr Cys Arg Asn Pro Asp Arg Glu Leu Arg	
130 135 140	
cct tgg tgt ttc acc acc gac ccc aac aag cgc tgg gaa ctt tgc gac	480
Pro Trp Cys Phe Thr Thr Asp Pro Asn Lys Arg Trp Glu Leu Cys Asp	
145 150 155 160	
atc ccc cgc tgc aca aca cct cca cca tct tct ggt ccc acc tac cag	528
Ile Pro Arg Cys Thr Thr Pro Pro Pro Ser Ser Gly Pro Thr Tyr Gln	
165 170 175	
tgt ctg aag gga aca ggt gaa aac tat cgc ggg aat gtg gct gtt acc	576
Cys Leu Lys Gly Thr Gly Glu Asn Tyr Arg Gly Asn Val Ala Val Thr	
180 185 190	
gtt tcc ggg cac acc tgt cag cac tgg agt gca cag acc cct cac aca	624
Val Ser Gly His Thr Cys Gln His Trp Ser Ala Gln Thr Pro His Thr	
195 200 205	
cat aac agg aca cca gaa aac ttc ccc tgc aaa aat ttg gat gaa aac	672
His Asn Arg Thr Pro Glu Asn Phe Pro Cys Lys Asn Leu Asp Glu Asn	
210 215 220	
tac tgc cgc aat cct gac gga aaa agg gcc cca tgg tgc cat aca acc	720
Tyr Cys Arg Asn Pro Asp Gly Lys Arg Ala Pro Trp Cys His Thr Thr	
225 230 235 240	
aac agc caa gtg cgg tgg gag tac tgt aag ata ccg tcc tgt gac tcc	768
Asn Ser Gln Val Arg Trp Glu Tyr Cys Lys Ile Pro Ser Cys Asp Ser	
245 250 255	
tcc cca gta tcc acg gaa caa ttg gct ccc aca gca cca cct gag cta	816
Ser Pro Val Ser Thr Glu Gln Leu Ala Pro Thr Ala Pro Pro Glu Leu	
260 265 270	
acc cct gtg gtc cag gac tgc tac cat ggt gat gga cag agc tac cga	864
Thr Pro Val Val Gln Asp Cys Tyr His Gly Asp Gly Gln Ser Tyr Arg	
275 280 285	
ggc aca tcc tcc acc acc acc aca gga aag aag tgt cag tct tgg tca	912
Gly Thr Ser Ser Thr Thr Thr Thr Gly Lys Lys Cys Gln Ser Trp Ser	
290 295 300	
tct atg aca cca cac cgg cac cag aag acc cca gaa aac tac cca aat	960
Ser Met Thr Pro His Arg His Gln Lys Thr Pro Glu Asn Tyr Pro Asn	
305 310 315 320	
gct ggc ctg aca atg aac tac tgc agg aat cca gat gcc gat aaa ggc	1008
Ala Gly Leu Thr Met Asn Tyr Cys Arg Asn Pro Asp Ala Asp Lys Gly	
325 330 335	
ccc tgg tgt ttt acc aca gac ccc agc gtc agg tgg gag tac tgc aac	1056
Pro Trp Cys Phe Thr Thr Asp Pro Ser Val Arg Trp Glu Tyr Cys Asn	

340 345 350 1083

ctg aaa aaa tgc tca gga aca gaa gcg  
 Leu Lys Lys Cys Ser Gly Thr Glu Ala  
 355 360

<210> 6  
 <211> 361  
 <212> PRT  
 <213> Homo sapiens

<400> 6

Tyr Leu Ser Glu Cys Lys Thr Gly Asn Gly Lys Asn Tyr Arg Gly Thr  
 1 5 10 15  
 Met Ser Lys Thr Lys Asn Gly Ile Thr Cys Gln Lys Trp Ser Ser Thr  
 20 25 30  
 Ser Pro His Arg Pro Arg Phe Ser Pro Ala Thr His Pro Ser Glu Gly  
 35 40 45  
 Leu Glu Glu Asn Tyr Cys Arg Asn Pro Asp Asn Asp Pro Gln Gly Pro  
 50 55 60  
 Trp Cys Tyr Thr Thr Asp Pro Glu Lys Arg Tyr Asp Tyr Cys Asp Ile  
 65 70 75 80  
 Leu Glu Cys Glu Glu Glu Cys Met His Cys Ser Gly Glu Asn Tyr Asp  
 85 90 95  
 Gly Lys Ile Ser Lys Thr Met Ser Gly Leu Glu Cys Gln Ala Trp Asp  
 100 105 110  
 Ser Gln Ser Pro His Ala His Gly Tyr Ile Pro Ser Lys Phe Pro Asn  
 115 120 125  
 Lys Asn Leu Lys Lys Asn Tyr Cys Arg Asn Pro Asp Arg Glu Leu Arg  
 130 135 140  
 Pro Trp Cys Phe Thr Thr Asp Pro Asn Lys Arg Trp Glu Leu Cys Asp  
 145 150 155 160  
 Ile Pro Arg Cys Thr Thr Pro Pro Pro Ser Ser Gly Pro Thr Tyr Gln  
 165 170 175  
 Cys Leu Lys Gly Thr Gly Glu Asn Tyr Arg Gly Asn Val Ala Val Thr  
 180 185 190  
 Val Ser Gly His Thr Cys Gln His Trp Ser Ala Gln Thr Pro His Thr  
 195 200 205  
 His Asn Arg Thr Pro Glu Asn Phe Pro Cys Lys Asn Leu Asp Glu Asn  
 210 215 220  
 Tyr Cys Arg Asn Pro Asp Gly Lys Arg Ala Pro Trp Cys His Thr Thr  
 225 230 235 240  
 Asn Ser Gln Val Arg Trp Glu Tyr Cys Lys Ile Pro Ser Cys Asp Ser  
 245 250 255  
 Ser Pro Val Ser Thr Glu Gln Leu Ala Pro Thr Ala Pro Pro Glu Leu  
 260 265 270  
 Thr Pro Val Val Gln Asp Cys Tyr His Gly Asp Gly Gln Ser Tyr Arg  
 275 280 285  
 Gly Thr Ser Ser Thr Thr Thr Thr Gly Lys Lys Cys Gln Ser Trp Ser  
 290 295 300  
 Ser Met Thr Pro His Arg His Gln Lys Thr Pro Glu Asn Tyr Pro Asn  
 305 310 315 320  
 Ala Gly Leu Thr Met Asn Tyr Cys Arg Asn Pro Asp Ala Asp Lys Gly  
 325 330 335

Pro Trp Cys Phe Thr Thr Asp Pro Ser Val Arg Trp Glu Tyr Cys Asn  
 340 345 350  
 Leu Lys Lys Cys Ser Gly Thr Glu Ala  
 355 360

<210> 7  
 <211> 1086  
 <212> DNA  
 <213> Mus musculus

<220>  
 <221> CDS  
 <222> (1)...(1086)

<400> 7

gtg tat ctg tca gaa tgt aag acc ggc atc ggc aac ggc tac aga gga	48
Val Tyr Leu Ser Glu Cys Lys Thr Gly Ile Gly Asn Gly Tyr Arg Gly	
1 5 10 15	
acc atg tcc agg aca aag agt ggt gtc gcc tgt caa aag tgg ggt gcc	96
Thr Met Ser Arg Thr Lys Ser Gly Val Ala Cys Gln Lys Trp Gly Ala	
20 25 30	
acg ttc ccc cac gta ccc aac tac tct ccc agt aca cat ccc aat gag	144
Thr Phe Pro His Val Pro Asn Tyr Ser Pro Ser Thr His Pro Asn Glu	
35 40 45	
gga cta gaa gag aac tac tgt agg aac cca gac aat gat gaa caa ggg	192
Gly Leu Glu Glu Asn Tyr Cys Arg Asn Pro Asp Asn Asp Glu Gln Gly	
50 55 60	
cct tgg tgc tac act aca gat ccg gac aag aga tat gac tac tgc aac	240
Pro Trp Cys Tyr Thr Thr Asp Pro Asp Lys Arg Tyr Asp Tyr Cys Asn	
65 70 75 80	
att cct gaa tgt gaa gag gaa tgc atg tac tgc agt gga gaa aag tat	288
Ile Pro Glu Cys Glu Glu Glu Cys Met Tyr Cys Ser Gly Glu Lys Tyr	
85 90 95	
gag ggc aaa atc tcc aag acc atg tct gga ctt gac tgc cag gcc tgg	336
Glu Gly Lys Ile Ser Lys Thr Met Ser Gly Leu Asp Cys Gln Ala Trp	
100 105 110	
gat tct cag agc cca cat gct cat gga tac atc cct gcc aaa ttt cca	384
Asp Ser Gln Ser Pro His Ala His Gly Tyr Ile Pro Ala Lys Phe Pro	
115 120 125	
agc aag aac ctg aag atg aat tat tgc cac aac cct gac ggg gag cca	432
Ser Lys Asn Leu Lys Met Asn Tyr Cys His Asn Pro Asp Gly Glu Pro	
130 135 140	
agg ccc tgg tgc ttc aca aca gac ccc acc aaa cgc tgg gaa tac tgt	480
Arg Pro Trp Cys Phe Thr Asp Pro Thr Lys Arg Trp Glu Tyr Cys	
145 150 155 160	

gac atc ccc cgc tgc aca aca ccc ccg ccc cca ccc agc cca acc tac 528  
 Asp Ile Pro Arg Cys Thr Thr Pro Pro Pro Pro Pro Ser Pro Thr Tyr  
 165 170 175

caa tgt ctg aaa gga aga ggt gaa aat tac cga ggg acc gtg tct gtc 576  
 Gln Cys Leu Lys Gly Arg Gly Glu Asn Tyr Arg Gly Thr Val Ser Val  
 180 185 190

acc gtg tct ggg aaa acc tgt cag cgc tgg agt gag caa acc cct cat 624  
 Thr Val Ser Gly Lys Thr Cys Gln Arg Trp Ser Glu Gln Thr Pro His  
 195 200 205

agg cac aac agg aca cca gaa aat ttc ccc tgc aaa aat ctg gaa gag 672  
 Arg His Asn Arg Thr Pro Glu Asn Phe Pro Cys Lys Asn Leu Glu Glu  
 210 215 220

aac tac tgc cgg aac cca gat gga gaa act gct ccc tgg tgc tat acc 720  
 Asn Tyr Cys Arg Asn Pro Asp Gly Glu Thr Ala Pro Trp Cys Tyr Thr  
 225 230 235 240

act gac agc cag ctg agg tgg gag tac tgt gag att cca tcc tgc gag 768  
 Thr Asp Ser Gln Leu Arg Trp Glu Tyr Cys Glu Ile Pro Ser Cys Glu  
 245 250 255

tcc tca gca tca cca gac cag tca gat tcc tca gtt cca cca gag gag 816  
 Ser Ser Ala Ser Pro Asp Gln Ser Asp Ser Ser Val Pro Pro Glu Glu  
 260 265 270

caa aca cct gtg gtc cag gaa tgc tac cag agc gat ggg cag agc tat 864  
 Gln Thr Pro Val Val Gln Glu Cys Tyr Gln Ser Asp Gly Gln Ser Tyr  
 275 280 285

cgg ggt aca tgc tcc act acc atc aca ggg aag aag tgc cag tcc tgg 912  
 Arg Gly Thr Ser Ser Thr Thr Ile Thr Gly Lys Lys Cys Gln Ser Trp  
 290 295 300

gca gct atg ttt cca cac agg cat tgc aag acc cca gag aac ttc cca 960  
 Ala Ala Met Phe Pro His Arg His Ser Lys Thr Pro Glu Asn Phe Pro  
 305 310 315 320

gat gct ggc ttg gag atg aac tac tgc agg aac ccg gat ggt gac aag 1008  
 Asp Ala Gly Leu Glu Met Asn Tyr Cys Arg Asn Pro Asp Gly Asp Lys  
 325 330 335

ggc cct tgg tgc tac acc act gac ccg agc gtc agg tgg gaa tac tgc 1056  
 Gly Pro Trp Cys Tyr Thr Thr Asp Pro Ser Val Arg Trp Glu Tyr Cys  
 340 345 350

aac ctg aag cgg tgc tca gag aca gga ggg 1086  
 Asn Leu Lys Arg Cys Ser Glu Thr Gly Gly  
 355 360

&lt;210&gt; 8

&lt;211&gt; 362

&lt;212&gt; PRT

&lt;213&gt; Mus musculus

&lt;400&gt; 8

```

Val Tyr Leu Ser Glu Cys Lys Thr Gly Ile Gly Asn Gly Tyr Arg Gly
 1           5           10           15
Thr Met Ser Arg Thr Lys Ser Gly Val Ala Cys Gln Lys Trp Gly Ala
 20           25           30
Thr Phe Pro His Val Pro Asn Tyr Ser Pro Ser Thr His Pro Asn Glu
 35           40           45
Gly Leu Glu Glu Asn Tyr Cys Arg Asn Pro Asp Asn Asp Glu Gln Gly
 50           55           60
Pro Trp Cys Tyr Thr Thr Asp Pro Asp Lys Arg Tyr Asp Tyr Cys Asn
 65           70           75           80
Ile Pro Glu Cys Glu Glu Cys Met Tyr Cys Ser Gly Glu Lys Tyr
 85           90           95
Glu Gly Lys Ile Ser Lys Thr Met Ser Gly Leu Asp Cys Gln Ala Trp
100           105           110
Asp Ser Gln Ser Pro His Ala His Gly Tyr Ile Pro Ala Lys Phe Pro
115           120           125
Ser Lys Asn Leu Lys Met Asn Tyr Cys His Asn Pro Asp Gly Glu Pro
130           135           140
Arg Pro Trp Cys Phe Thr Thr Asp Pro Thr Lys Arg Trp Glu Tyr Cys
145           150           155           160
Asp Ile Pro Arg Cys Thr Thr Pro Pro Pro Pro Ser Pro Thr Tyr
165           170           175
Gln Cys Leu Lys Gly Arg Gly Glu Asn Tyr Arg Gly Thr Val Ser Val
180           185           190
Thr Val Ser Gly Lys Thr Cys Gln Arg Trp Ser Glu Gln Thr Pro His
195           200           205
Arg His Asn Arg Thr Pro Glu Asn Phe Pro Cys Lys Asn Leu Glu Glu
210           215           220
Asn Tyr Cys Arg Asn Pro Asp Gly Glu Thr Ala Pro Trp Cys Tyr Thr
225           230           235           240
Thr Asp Ser Gln Leu Arg Trp Glu Tyr Cys Glu Ile Pro Ser Cys Glu
245           250           255
Ser Ser Ala Ser Pro Asp Gln Ser Asp Ser Ser Val Pro Pro Glu Glu
260           265           270
Gln Thr Pro Val Val Gln Glu Cys Tyr Gln Ser Asp Gly Gln Ser Tyr
275           280           285
Arg Gly Thr Ser Ser Thr Thr Ile Thr Gly Lys Lys Cys Gln Ser Trp
290           295           300
Ala Ala Met Phe Pro His Arg His Ser Lys Thr Pro Glu Asn Phe Pro
305           310           315           320
Asp Ala Gly Leu Glu Met Asn Tyr Cys Arg Asn Pro Asp Gly Asp Lys
325           330           335
Gly Pro Trp Cys Tyr Thr Thr Asp Pro Ser Val Arg Trp Glu Tyr Cys
340           345           350
Asn Leu Lys Arg Cys Ser Glu Thr Gly Gly
355           360

```

&lt;210&gt; 9

&lt;211&gt; 552

&lt;212&gt; DNA

&lt;213&gt; Mus musculus

<220>  
 <221> CDS  
 <222> (1) ... (552)

<400> 9  
 cat act cat cag gac ttt cag cca gtg ctc cac ctg gtg gca ctg aac 48  
 His Thr His Gln Asp Phe Gln Pro Val Leu His Leu Val Ala Leu Asn  
 1 5 10 15  
 acc ccc ctg tct gga ggc atg cgt ggt atc cgt gga gca gat ttc cag 96  
 Thr Pro Leu Ser Gly Gly Met Arg Gly Ile Arg Gly Ala Asp Phe Gln  
 20 25 30  
 tgc ttc cag caa gcc cga gcc gtg ggg ctg tcg ggc acc ttc cgg gct 144  
 Cys Phe Gln Gln Ala Arg Ala Val Gly Leu Ser Gly Thr Phe Arg Ala  
 35 40 45  
 ttc ctg tcc tct agg ctg cag gat ctc tat agc atc gtg cgc cgt gct 192  
 Phe Leu Ser Ser Arg Leu Gln Asp Leu Tyr Ser Ile Val Arg Arg Ala  
 50 55 60  
 gac cgg ggg tct gtg ccc atc gtc aac ctg aag gac gag gtg cta tct 240  
 Asp Arg Gly Ser Val Pro Ile Val Asn Leu Lys Asp Glu Val Leu Ser  
 65 70 75 80  
 ccc agc tgg gac tcc ctg ttt tct ggc tcc cag ggt caa gtg caa ccc 288  
 Pro Ser Trp Asp Ser Leu Phe Ser Gly Ser Gln Gly Gln Val Gln Pro  
 85 90 95  
 ggg gcc cgc atc ttt tct ttt gac ggc aga gat gtc ctg aga cac cca 336  
 Gly Ala Arg Ile Phe Ser Phe Asp Gly Arg Asp Val Leu Arg His Pro  
 100 105 110  
 gcc tgg ccg cag aag agc gta tgg cac ggc tcg gac ccc agt ggg cgg 384  
 Ala Trp Pro Gln Lys Ser Val Trp His Gly Ser Asp Pro Ser Gly Arg  
 115 120 125  
 agg ctg atg gag agt tac tgt gag aca tgg cga act gaa act act ggg 432  
 Arg Leu Met Glu Ser Tyr Cys Glu Thr Trp Arg Thr Glu Thr Thr Gly  
 130 135 140  
 gct aca ggt cag gcc tcc tcc ctg ctg tca ggc agg ctc ctg gaa cag 480  
 Ala Thr Gly Gln Ala Ser Ser Leu Leu Ser Gly Arg Leu Leu Glu Gln  
 145 150 155 160  
 aaa gct gcg agc tgc cac aac agc tac atc gtc ctg tgc att gag aat 528  
 Lys Ala Ala Ser Cys His Asn Ser Tyr Ile Val Leu Cys Ile Glu Asn  
 165 170 175  
 agc ttc atg acc tct ttc tcc aaa 552  
 Ser Phe Met Thr Ser Phe Ser Lys  
 180

<210> 10

<211> 184  
 <212> PRT  
 <213> Mus musculus

©

<400> 10  
 His Thr His Gln Asp Phe Gln Pro Val Leu His Leu Val Ala Leu Asn  
 1 5 10 15  
 Thr Pro Leu Ser Gly Gly Met Arg Gly Ile Arg Gly Ala Asp Phe Gln  
 20 25 30  
 Cys Phe Gln Gln Ala Arg Ala Val Gly Leu Ser Gly Thr Phe Arg Ala  
 35 40 45  
 Phe Leu Ser Ser Arg Leu Gln Asp Leu Tyr Ser Ile Val Arg Arg Ala  
 50 55 60  
 Asp Arg Gly Ser Val Pro Ile Val Asn Leu Lys Asp Glu Val Leu Ser  
 65 70 75 80  
 Pro Ser Trp Asp Ser Leu Phe Ser Gly Ser Gln Gly Gln Val Gln Pro  
 85 90 95  
 Gly Ala Arg Ile Phe Ser Phe Asp Gly Arg Asp Val Leu Arg His Pro  
 100 105 110  
 Ala Trp Pro Gln Lys Ser Val Trp His Gly Ser Asp Pro Ser Gly Arg  
 115 120 125  
 Arg Leu Met Glu Ser Tyr Cys Glu Thr Trp Arg Thr Glu Thr Thr Gly  
 130 135 140  
 Ala Thr Gly Gln Ala Ser Ser Leu Leu Ser Gly Arg Leu Leu Glu Gln  
 145 150 155 160  
 Lys Ala Ala Ser Cys His Asn Ser Tyr Ile Val Leu Cys Ile Glu Asn  
 165 170 175  
 Ser Phe Met Thr Ser Phe Ser Lys  
 180

<210> 11  
 <211> 1414  
 <212> DNA  
 <213> Mus musculus

<220>  
 <221> CDS  
 <222> (1) ... (1414)

<400> 11  
 atg gac cat aag gaa gta atc ctt ctg ttt ctc ttg ctt ctg aaa cca 48  
 Met Asp His Lys Glu Val Ile Leu Leu Phe Leu Leu Leu Leu Lys Pro  
 1 5 10 15  
 gga caa ggg gac tcg ctg gat ggc tac ata agc aca caa ggg gct tca 96  
 Gly Gln Gly Asp Ser Leu Asp Gly Tyr Ile Ser Thr Gln Gly Ala Ser  
 20 25 30  
 ctg ttc agt ctc acc aag aag cag ctc gca gca gga ggt gtc tcg gac 144  
 Leu Phe Ser Leu Thr Lys Lys Gln Leu Ala Ala Gly Gly Val Ser Asp  
 35 40 45  
 tgt ttg gcc aaa tgt gaa ggg gaa aca gac ttt gtc tgc agg tca ttc 192  
 Cys Leu Ala Lys Cys Glu Gly Glu Thr Asp Phe Val Cys Arg Ser Phe  
 50 55 60



cag tac cac agc aaa gag cag caa tgc gtg atc atg gcg gag aac agc Gln Tyr His Ser Lys Glu Gln Gln Cys Val Ile Met Ala Glu Asn Ser 65 70 75 80	240
aag act tcc tcc atc atc cgg atg aga gac gtc atc tta ttc gaa aag Lys Thr Ser Ser Ile Ile Arg Met Arg Asp Val Ile Leu Phe Glu Lys 85 90 95	288
aga gtg tat ctg tca gaa tgt aag acc ggc atc ggc aac ggc tac aga Arg Val Tyr Leu Ser Glu Cys Lys Thr Gly Ile Gly Asn Gly Tyr Arg 100 105 110	336
gga acc atg tcc agg aca aag agt ggt gtt gcc tgt caa aag tgg ggt Gly Thr Met Ser Arg Thr Lys Ser Gly Val Ala Cys Gln Lys Trp Gly 115 120 125	384
gcc acg ttc ccc cac gta ccc aac tac tct ccc agt aca cat ccc aat Ala Thr Phe Pro His Val Pro Asn Tyr Ser Pro Ser Thr His Pro Asn 130 135 140	432
gag gga cta gaa gag aac tac tgt agg aac cca gac aat gat gaa caa Glu Gly Leu Glu Glu Asn Tyr Cys Arg Asn Pro Asp Asn Asp Glu Gln 145 150 155 160	480
ggg cct tgg tgc tac act aca gat ccg gac aag aga tat gac tac tgc Gly Pro Trp Cys Tyr Thr Thr Asp Pro Asp Lys Arg Tyr Asp Tyr Cys 165 170 175	528
aac att cct gaa tgt gaa gag gaa tgc atg tac tgc agt gga gaa aag Asn Ile Pro Glu Cys Glu Glu Glu Cys Met Tyr Cys Ser Gly Glu Lys 180 185 190	576
tat gag ggc aaa atc tcc aag acc atg tct gga ctt gac tgc cag gcc Tyr Glu Gly Lys Ile Ser Lys Thr Met Ser Gly Leu Asp Cys Gln Ala 195 200 205	624
tgg gat tct cag agc cca cat gct cat gga tac atc cct gcc aaa ttt Trp Asp Ser Gln Ser Pro His Ala His Gly Tyr Ile Pro Ala Lys Phe 210 215 220	672
cca agc aag aac ctg aag atg aat tat tgc cac aac cct gac ggg gag Pro Ser Lys Asn Leu Lys Met Asn Tyr Cys His Asn Pro Asp Gly Glu 225 230 235 240	720
cca agg ccc tgg tgc ttc aca aca gac ccc acc aaa cgc tgg gaa tac Pro Arg Pro Trp Cys Phe Thr Thr Asp Pro Thr Lys Arg Trp Glu Tyr 245 250 255	768
tgt gac atc ccc cgc tgc aca aca ccc ccg ccc cca ccc agc cca acc Cys Asp Ile Pro Arg Cys Thr Thr Pro Pro Pro Pro Pro Ser Pro Thr 260 265 270	816
tac caa tgt ctg aaa gga aga ggt gaa aat tac cga ggg acc gtg tct Tyr Gln Cys Leu Lys Gly Arg Gly Glu Asn Tyr Arg Gly Thr Val Ser	864

275	280	285	
gtc acc gtg tct ggg aaa acc tgt cag cgc tgg agt gag caa acc cct			912
Val Thr Val Ser Gly Lys Thr Cys Gln Arg Trp Ser Glu Gln Thr Pro			
290	295	300	
cat agg cac aac agg aca cca gaa aat ttc ccc tgc aaa aat ctg gaa			960
His Arg His Asn Arg Thr Pro Glu Asn Phe Pro Cys Lys Asn Leu Glu			
305	310	315	320
gag aac tac tgc cgg aac cca gat gga gaa act gct ccc tgg tgc tat			1008
Glu Asn Tyr Cys Arg Asn Pro Asp Gly Glu Thr Ala Pro Trp Cys Tyr			
325	330	335	
acc act gac agc cag ctg agg tgg gag tac tgt gag att cca tcc tgc			1056
Thr Thr Asp Ser Gln Leu Arg Trp Glu Tyr Cys Glu Ile Pro Ser Cys			
340	345	350	
gag tcc tca gca tca cca gac cag tca gat tcc tca gtt cca cca gag			1104
Glu Ser Ser Ala Ser Pro Asp Gln Ser Asp Ser Ser Val Pro Pro Glu			
355	360	365	
gag caa aca cct gtg gtc cag gaa tgc tac cag agc gat ggg cag agc			1152
Glu Gln Thr Pro Val Val Gln Glu Cys Tyr Gln Ser Asp Gly Gln Ser			
370	375	380	
tat cgg ggt aca tcg tcc act acc atc aca ggg aag aag tgc cag tcc			1200
Tyr Arg Gly Thr Ser Ser Thr Thr Ile Thr Gly Lys Lys Cys Gln Ser			
385	390	395	400
tgg gca gct atg ttt cca cac agg cat tcg aag acc cca gag aac ttc			1248
Trp Ala Ala Met Phe Pro His Arg His Ser Lys Thr Pro Glu Asn Phe			
405	410	415	
cca gat gct ggc ttg gag atg aac tac tgc agg aac ccg gat ggt gac			1296
Pro Asp Ala Gly Leu Glu Met Asn Tyr Cys Arg Asn Pro Asp Gly Asp			
420	425	430	
aag ggc cct tgg tgc tac acc act gac ccg agc gtc agg tgg gaa tac			1344
Lys Gly Pro Trp Cys Tyr Thr Thr Asp Pro Ser Val Arg Trp Glu Tyr			
435	440	445	
tgc aac ctg aag cgg tgc tca gag aca gga ggg aat tca gac tac aag			1392
Cys Asn Leu Lys Arg Cys Ser Glu Thr Gly Gly Asn Ser Asp Tyr Lys			
450	455	460	
gac gac gat gac aag taa taa c			1414
Asp Asp Asp Asp Lys * *			
465			

<210> 12  
 <211> 469  
 <212> PRT  
 <213> Mus musculus

<400> 12

Met	Asp	His	Lys	Glu	Val	Ile	Leu	Leu	Phe	Leu	Leu	Leu	Leu	Lys	Pro
1				5					10					15	
Gly	Gln	Gly	Asp	Ser	Leu	Asp	Gly	Tyr	Ile	Ser	Thr	Gln	Gly	Ala	Ser
			20					25					30		
Leu	Phe	Ser	Leu	Thr	Lys	Lys	Gln	Leu	Ala	Ala	Gly	Gly	Val	Ser	Asp
		35					40					45			
Cys	Leu	Ala	Lys	Cys	Glu	Gly	Glu	Thr	Asp	Phe	Val	Cys	Arg	Ser	Phe
	50					55					60				
Gln	Tyr	His	Ser	Lys	Glu	Gln	Gln	Cys	Val	Ile	Met	Ala	Glu	Asn	Ser
65					70					75				80	
Lys	Thr	Ser	Ser	Ile	Ile	Arg	Met	Arg	Asp	Val	Ile	Leu	Phe	Glu	Lys
			85						90					95	
Arg	Val	Tyr	Leu	Ser	Glu	Cys	Lys	Thr	Gly	Ile	Gly	Asn	Gly	Tyr	Arg
			100						105				110		
Gly	Thr	Met	Ser	Arg	Thr	Lys	Ser	Gly	Val	Ala	Cys	Gln	Lys	Trp	Gly
		115					120					125			
Ala	Thr	Phe	Pro	His	Val	Pro	Asn	Tyr	Ser	Pro	Ser	Thr	His	Pro	Asn
	130					135					140				
Glu	Gly	Leu	Glu	Glu	Asn	Tyr	Cys	Arg	Asn	Pro	Asp	Asn	Asp	Glu	Gln
145					150					155				160	
Gly	Pro	Trp	Cys	Tyr	Thr	Thr	Asp	Pro	Asp	Lys	Arg	Tyr	Asp	Tyr	Cys
			165						170				175		
Asn	Ile	Pro	Glu	Cys	Glu	Glu	Glu	Cys	Met	Tyr	Cys	Ser	Gly	Glu	Lys
		180						185				190			
Tyr	Glu	Gly	Lys	Ile	Ser	Lys	Thr	Met	Ser	Gly	Leu	Asp	Cys	Gln	Ala
	195						200					205			
Trp	Asp	Ser	Gln	Ser	Pro	His	Ala	His	Gly	Tyr	Ile	Pro	Ala	Lys	Phe
	210					215					220				
Pro	Ser	Lys	Asn	Leu	Lys	Met	Asn	Tyr	Cys	His	Asn	Pro	Asp	Gly	Glu
225				230						235				240	
Pro	Arg	Pro	Trp	Cys	Phe	Thr	Thr	Asp	Pro	Thr	Lys	Arg	Trp	Glu	Tyr
			245						250				255		
Cys	Asp	Ile	Pro	Arg	Cys	Thr	Thr	Pro	Pro	Pro	Pro	Pro	Ser	Pro	Thr
		260						265					270		
Tyr	Gln	Cys	Leu	Lys	Gly	Arg	Gly	Glu	Asn	Tyr	Arg	Gly	Thr	Val	Ser
	275						280					285			
Val	Thr	Val	Ser	Gly	Lys	Thr	Cys	Gln	Arg	Trp	Ser	Glu	Gln	Thr	Pro
	290					295					300				
His	Arg	His	Asn	Arg	Thr	Pro	Glu	Asn	Phe	Pro	Cys	Lys	Asn	Leu	Glu
305					310					315				320	
Glu	Asn	Tyr	Cys	Arg	Asn	Pro	Asp	Gly	Glu	Thr	Ala	Pro	Trp	Cys	Tyr
			325						330				335		
Thr	Thr	Asp	Ser	Gln	Leu	Arg	Trp	Glu	Tyr	Cys	Glu	Ile	Pro	Ser	Cys
		340						345				350			
Glu	Ser	Ser	Ala	Ser	Pro	Asp	Gln	Ser	Asp	Ser	Ser	Val	Pro	Pro	Glu
		355					360					365			
Glu	Gln	Thr	Pro	Val	Val	Gln	Glu	Cys	Tyr	Gln	Ser	Asp	Gly	Gln	Ser
	370					375					380				
Tyr	Arg	Gly	Thr	Ser	Ser	Thr	Thr	Ile	Thr	Gly	Lys	Lys	Cys	Gln	Ser
385					390					395				400	
Trp	Ala	Ala	Met	Phe	Pro	His	Arg	His	Ser	Lys	Thr	Pro	Glu	Asn	Phe
			405						410				415		
Pro	Asp	Ala	Gly	Leu	Glu	Met	Asn	Tyr	Cys	Arg	Asn	Pro	Asp	Gly	Asp
			420					425					430		

Lys Gly Pro Trp Cys Tyr Thr Thr Asp Pro Ser Val Arg Trp Glu Tyr  
 435 440 445  
 Cys Asn Leu Lys Arg Cys Ser Glu Thr Gly Gly Asn Ser Asp Tyr Lys  
 450 455 460  
 Asp Asp Asp Asp Lys  
 465

<210> 13  
 <211> 661  
 <212> DNA  
 <213> Mus musculus

<220>  
 <221> CDS  
 <222> (1)...(661)

<400> 13  
 atg gac cat aag gaa gta atc ctt ctg ttt ctc ttg ctt ctg aaa cca 48  
 Met Asp His Lys Glu Val Ile Leu Leu Phe Leu Leu Leu Lys Pro  
 1 5 10 15  
 gga caa ggg gac tcg cta gat ctt gac tac aag gac gac gat gac aag 96  
 Gly Gln Gly Asp Ser Leu Asp Leu Asp Tyr Lys Asp Asp Asp Asp Lys  
 20 25 30  
 ctt gct cat act cat cag gac ttt cag cca gtg ctc cac ctg gtg gca 144  
 Leu Ala His Thr His Gln Asp Phe Gln Pro Val Leu His Leu Val Ala  
 35 40 45  
 ctg aac acc ccc ctg tct gga ggc atg cgt ggt atc cgt gga gca gat 192  
 Leu Asn Thr Pro Leu Ser Gly Gly Met Arg Gly Ile Arg Gly Ala Asp  
 50 55 60  
 ttc cag tgc ttc cag caa gcc cga gcc gtg ggg ctg tcg ggc acc ttc 240  
 Phe Gln Cys Phe Gln Gln Ala Arg Ala Val Gly Leu Ser Gly Thr Phe  
 65 70 75 80  
 cgg gct ttc ctg tcc tct agg ctg cag gat ctc tat agc atc gtg cgc 288  
 Arg Ala Phe Leu Ser Ser Arg Leu Gln Asp Leu Tyr Ser Ile Val Arg  
 85 90 95  
 cgt gct gac cgg ggg tct gtg ccc atc gtc aac ctg aag gac gag gtg 336  
 Arg Ala Asp Arg Gly Ser Val Pro Ile Val Asn Leu Lys Asp Glu Val  
 100 105 110  
 cta tct ccc agc tgg gac tcc ctg ttt tct ggc tcc cag ggt caa gtg 384  
 Leu Ser Pro Ser Trp Asp Ser Leu Phe Ser Gly Ser Gln Gly Gln Val  
 115 120 125  
 caa ccc ggg gcc cgc atc ttt tct ttt gac ggc aga gat gtc ctg aga 432  
 Gln Pro Gly Ala Arg Ile Phe Ser Phe Asp Gly Arg Asp Val Leu Arg  
 130 135 140  
 cac cca gcc tgg ccg cag aag agc gta tgg cac ggc tcg gac ccc agt 480  
 His Pro Ala Trp Pro Gln Lys Ser Val Trp His Gly Ser Asp Pro Ser

```

145              150              155              160
ggg cgg agg ctg atg gag agt tac tgt gag aca tgg cga act gaa act      528
Gly Arg Arg Leu Met Glu Ser Tyr Cys Glu Thr Trp Arg Thr Glu Thr
              165              170              175

act ggg gct aca ggt cag gcc tcc tcc ctg ctg tca ggc agg ctc ctg      576
Thr Gly Ala Thr Gly Gln Ala Ser Ser Leu Leu Ser Gly Arg Leu Leu
              180              185              190

gaa cag aaa gct gcg agc tgc cac aac agc tac atc gtc ctg tgc att      624
Glu Gln Lys Ala Ala Ser Cys His Asn Ser Tyr Ile Val Leu Cys Ile
              195              200              205

gag aat agc ttc atg acc tct ttc tcc aaa taa taa c      661
Glu Asn Ser Phe Met Thr Ser Phe Ser Lys * *
              210              215

```

```

<210> 14
<211> 218
<212> PRT
<213> Mus musculus

```

```

<400> 14
Met Asp His Lys Glu Val Ile Leu Leu Phe Leu Leu Leu Leu Lys Pro
 1              5              10              15
Gly Gln Gly Asp Ser Leu Asp Leu Asp Tyr Lys Asp Asp Asp Asp Lys
              20              25              30
Leu Ala His Thr His Gln Asp Phe Gln Pro Val Leu His Leu Val Ala
              35              40              45
Leu Asn Thr Pro Leu Ser Gly Gly Met Arg Gly Ile Arg Gly Ala Asp
              50              55              60
Phe Gln Cys Phe Gln Gln Ala Arg Ala Val Gly Leu Ser Gly Thr Phe
              65              70              75              80
Arg Ala Phe Leu Ser Ser Arg Leu Gln Asp Leu Tyr Ser Ile Val Arg
              85              90              95
Arg Ala Asp Arg Gly Ser Val Pro Ile Val Asn Leu Lys Asp Glu Val
              100              105              110
Leu Ser Pro Ser Trp Asp Ser Leu Phe Ser Gly Ser Gln Gly Gln Val
              115              120              125
Gln Pro Gly Ala Arg Ile Phe Ser Phe Asp Gly Arg Asp Val Leu Arg
              130              135              140
His Pro Ala Trp Pro Gln Lys Ser Val Trp His Gly Ser Asp Pro Ser
              145              150              155              160
Gly Arg Arg Leu Met Glu Ser Tyr Cys Glu Thr Trp Arg Thr Glu Thr
              165              170              175
Thr Gly Ala Thr Gly Gln Ala Ser Ser Leu Leu Ser Gly Arg Leu Leu
              180              185              190
Glu Gln Lys Ala Ala Ser Cys His Asn Ser Tyr Ile Val Leu Cys Ile
              195              200              205
Glu Asn Ser Phe Met Thr Ser Phe Ser Lys
              210              215

```

```

<210> 15

```

<211> 1747  
 <212> DNA  
 <213> Mus musculus

<220>  
 <221> CDS  
 <222> (1)...(1747)

```

<400> 15
atg gac cat aag gaa gta atc ctt ctg ttt ctc ttg ctt ctg aaa cca      48
Met Asp His Lys Glu Val Ile Leu Leu Phe Leu Leu Leu Leu Lys Pro
1          5          10          15

gga caa ggg gac tcg ctg gat ggc tac ata agc aca caa ggg gct tca      96
Gly Gln Gly Asp Ser Leu Asp Gly Tyr Ile Ser Thr Gln Gly Ala Ser
          20          25          30

ctg ttc agt ctc acc aag aag cag ctc gca gca gga ggt gtc tcg gac     144
Leu Phe Ser Leu Thr Lys Lys Gln Leu Ala Ala Gly Gly Val Ser Asp
          35          40          45

tgt ttg gcc aaa tgt gaa ggg gaa aca gac ttt gtc tgc agg tca ttc     192
Cys Leu Ala Lys Cys Glu Gly Glu Thr Asp Phe Val Cys Arg Ser Phe
          50          55          60

cag tac cac agc aaa gag cag caa tgc gtg atc atg gcg gag aac agc     240
Gln Tyr His Ser Lys Glu Gln Gln Cys Val Ile Met Ala Glu Asn Ser
          65          70          75          80

aag act tcc tcc atc atc cgg atg aga gac gtc atc tta ttc gaa aag     288
Lys Thr Ser Ser Ile Ile Arg Met Arg Asp Val Ile Leu Phe Glu Lys
          85          90          95

aga gtg tat ctg tca gaa tgt aag acc ggc atc ggc aac ggc tac aga     336
Arg Val Tyr Leu Ser Glu Cys Lys Thr Gly Ile Gly Asn Gly Tyr Arg
          100          105          110

gga acc atg tcc agg aca aag agt ggt gtt gcc tgt caa aag tgg ggt     384
Gly Thr Met Ser Arg Thr Lys Ser Gly Val Ala Cys Gln Lys Trp Gly
          115          120          125

gcc acg ttc ccc cac gta ccc aac tac tct ccc agt aca cat ccc aat     432
Ala Thr Phe Pro His Val Pro Asn Tyr Ser Pro Ser Thr His Pro Asn
          130          135          140

gag gga cta gaa gag aac tac tgt agg aac cca gac aat gat gaa caa     480
Glu Gly Leu Glu Glu Asn Tyr Cys Arg Asn Pro Asp Asn Asp Glu Gln
          145          150          155          160

ggg cct tgg tgc tac act aca gat ccg gac aag aga tat gac tac tgc     528
Gly Pro Trp Cys Tyr Thr Thr Asp Pro Asp Lys Arg Tyr Asp Tyr Cys
          165          170          175

aac att cct gaa tgt gaa gag gaa tgc atg tac tgc agt gga gaa aag     576
Asn Ile Pro Glu Cys Glu Glu Glu Cys Met Tyr Cys Ser Gly Glu Lys

```

180	185	190	
tat gag ggc aaa atc tcc aag acc atg tct gga ctt gac tgc cag gcc			624
Tyr Glu Gly Lys Ile Ser Lys Thr Met Ser Gly Leu Asp Cys Gln Ala			
195	200	205	
tgg gat tct cag agc cca cat gct cat gga tac atc cct gcc aaa ttt			672
Trp Asp Ser Gln Ser Pro His Ala His Gly Tyr Ile Pro Ala Lys Phe			
210	215	220	
cca agc aag aac ctg aag atg aat tat tgc cac aac cct gac ggg gag			720
Pro Ser Lys Asn Leu Lys Met Asn Tyr Cys His Asn Pro Asp Gly Glu			
225	230	235	240
cca agg ccc tgg tgc ttc aca aca gac ccc acc aaa cgc tgg gaa tac			768
Pro Arg Pro Trp Cys Phe Thr Thr Asp Pro Thr Lys Arg Trp Glu Tyr			
245	250	255	
tgt gac atc ccc cgc tgc aca aca ccc ccg ccc cca ccc agc cca acc			816
Cys Asp Ile Pro Arg Cys Thr Thr Pro Pro Pro Pro Pro Ser Pro Thr			
260	265	270	
tac caa tgt ctg aaa gga aga ggt gaa aat tac cga ggg acc gtg tct			864
Tyr Gln Cys Leu Lys Gly Arg Gly Glu Asn Tyr Arg Gly Thr Val Ser			
275	280	285	
gtc acc gtg tct ggg aaa acc tgt cag cgc tgg agt gag caa acc cct			912
Val Thr Val Ser Gly Lys Thr Cys Gln Arg Trp Ser Glu Gln Thr Pro			
290	295	300	
cat agg cac aac agg aca cca gaa aat ttc ccc tgc aaa aat ctg gaa			960
His Arg His Asn Arg Thr Pro Glu Asn Phe Pro Cys Lys Asn Leu Glu			
305	310	315	320
gag aac tac tgc cgg aac cca gat gga gaa act gct ccc tgg tgc tat			1008
Glu Asn Tyr Cys Arg Asn Pro Asp Gly Glu Thr Ala Pro Trp Cys Tyr			
325	330	335	
acc act gac agc cag ctg agg tgg gag tac tgt gag att cca tcc tgc			1056
Thr Thr Asp Ser Gln Leu Arg Trp Glu Tyr Cys Glu Ile Pro Ser Cys			
340	345	350	
gag tcc tca gca tca cca gac cag tca gat tcc tca gtt cca cca gag			1104
Glu Ser Ser Ala Ser Pro Asp Gln Ser Asp Ser Ser Val Pro Pro Glu			
355	360	365	
gag caa aca cct gtg gga ggg aat tgc ggc ggt gga tca ggt ggc gga			1152
Glu Gln Thr Pro Val Gly Gly Asn Cys Gly Gly Gly Ser Gly Gly Gly			
370	375	380	
gat ctt gac tac aag gac gac gat gac aag ctt gct cat act cat cag			1200
Asp Leu Asp Tyr Lys Asp Asp Asp Asp Lys Leu Ala His Thr His Gln			
385	390	395	400
gac ttt cag cca gtg ctc cac ctg gtg gca ctg aac acc ccc ctg tct			1248

Asp Phe Gln Pro Val Leu His Leu Val Ala Leu Asn Thr Pro Leu Ser	
405 410 415	
gga ggc atg cgt ggt atc cgt gga gca gat ttc cag tgc ttc cag caa	1296
Gly Gly Met Arg Gly Ile Arg Gly Ala Asp Phe Gln Cys Phe Gln Gln	
420 425 430	
gcc cga gcc gtg ggg ctg tgg ggc acc ttc cgg gct ttc ctg tcc tct	1344
Ala Arg Ala Val Gly Leu Ser Gly Thr Phe Arg Ala Phe Leu Ser Ser	
435 440 445	
agg ctg cag gat ctc tat agc atc gtg cgc cgt gct gac cgg ggg tct	1392
Arg Leu Gln Asp Leu Tyr Ser Ile Val Arg Arg Ala Asp Arg Gly Ser	
450 455 460	
gtg ccc atc gtc aac ctg aag gac gag gtg cta tct ccc agc tgg gac	1440
Val Pro Ile Val Asn Leu Lys Asp Glu Val Leu Ser Pro Ser Trp Asp	
465 470 475 480	
tcc ctg ttt tct ggc tcc cag ggt caa gtg caa ccc ggg gcc cgc atc	1488
Ser Leu Phe Ser Gly Ser Gln Gly Gln Val Gln Pro Gly Ala Arg Ile	
485 490 495	
ttt tct ttt gac ggc aga gat gtc ctg aga cac cca gcc tgg ccg cag	1536
Phe Ser Phe Asp Gly Arg Asp Val Leu Arg His Pro Ala Trp Pro Gln	
500 505 510	
aag agc gta tgg cac ggc tgg gac ccc agt ggg cgg agg ctg atg gag	1584
Lys Ser Val Trp His Gly Ser Asp Pro Ser Gly Arg Arg Leu Met Glu	
515 520 525	
agt tac tgt gag aca tgg cga act gaa act act ggg gct aca ggt cag	1632
Ser Tyr Cys Glu Thr Trp Arg Thr Glu Thr Thr Gly Ala Thr Gly Gln	
530 535 540	
gcc tcc tcc ctg ctg tca ggc agg ctc ctg gaa cag aaa gct gcg agc	1680
Ala Ser Ser Leu Leu Ser Gly Arg Leu Leu Glu Gln Lys Ala Ala Ser	
545 550 555 560	
tgc cac aac agc tac atc gtc ctg tgc att gag aat agc ttc atg acc	1728
Cys His Asn Ser Tyr Ile Val Leu Cys Ile Glu Asn Ser Phe Met Thr	
565 570 575	
tct ttc tcc aaa taa taa c	1747
Ser Phe Ser Lys * *	
580	

<210> 16  
 <211> 580  
 <212> PRT  
 <213> Mus musculus

<400> 16  
 Met Asp His Lys Glu Val Ile Leu Leu Phe Leu Leu Leu Lys Pro



1	5	10	15
Gly Gln Gly Asp Ser Leu Asp Gly Tyr Ile Ser Thr Gln Gly Ala Ser			
20	25	30	
Leu Phe Ser Ser Leu Thr Lys Lys Gln Leu Ala Ala Gly Gly Val Ser Asp			
35	40	45	
Cys Leu Ala Lys Cys Glu Gly Glu Thr Asp Phe Val Cys Arg Ser Phe			
50	55	60	
Gln Tyr His Ser Lys Glu Gln Gln Cys Val Ile Met Ala Glu Asn Ser			
65	70	75	80
Lys Thr Ser Ser Ile Ile Arg Met Arg Asp Val Ile Leu Phe Glu Lys			
85	90	95	
Arg Val Tyr Leu Ser Glu Cys Lys Thr Gly Ile Gly Asn Gly Tyr Arg			
100	105	110	
Gly Thr Met Ser Arg Thr Lys Ser Gly Val Ala Cys Gln Lys Trp Gly			
115	120	125	
Ala Thr Phe Pro His Val Pro Asn Tyr Ser Pro Ser Thr His Pro Asn			
130	135	140	
Glu Gly Leu Glu Glu Asn Tyr Cys Arg Asn Pro Asp Asn Asp Glu Gln			
145	150	155	160
Gly Pro Trp Cys Tyr Thr Thr Asp Pro Asp Lys Arg Tyr Asp Tyr Cys			
165	170	175	
Asn Ile Pro Glu Cys Glu Glu Glu Cys Met Tyr Cys Ser Gly Glu Lys			
180	185	190	
Tyr Glu Gly Lys Ile Ser Lys Thr Met Ser Gly Leu Asp Cys Gln Ala			
195	200	205	
Trp Asp Ser Gln Ser Pro His Ala His Gly Tyr Ile Pro Ala Lys Phe			
210	215	220	
Pro Ser Lys Asn Leu Lys Met Asn Tyr Cys His Asn Pro Asp Gly Glu			
225	230	235	240
Pro Arg Pro Trp Cys Phe Thr Thr Asp Pro Thr Lys Arg Trp Glu Tyr			
245	250	255	
Cys Asp Ile Pro Arg Cys Thr Thr Pro Pro Pro Pro Ser Pro Thr			
260	265	270	
Tyr Gln Cys Leu Lys Gly Arg Gly Glu Asn Tyr Arg Gly Thr Val Ser			
275	280	285	
Val Thr Val Ser Gly Lys Thr Cys Gln Arg Trp Ser Glu Gln Thr Pro			
290	295	300	
His Arg His Asn Arg Thr Pro Glu Asn Phe Pro Cys Lys Asn Leu Glu			
305	310	315	320
Glu Asn Tyr Cys Arg Asn Pro Asp Gly Glu Thr Ala Pro Trp Cys Tyr			
325	330	335	
Thr Thr Asp Ser Gln Leu Arg Trp Glu Tyr Cys Glu Ile Pro Ser Cys			
340	345	350	
Glu Ser Ser Ala Ser Pro Asp Gln Ser Asp Ser Ser Val Pro Pro Glu			
355	360	365	
Glu Gln Thr Pro Val Gly Gly Asn Cys Gly Gly Gly Ser Gly Gly Gly			
370	375	380	
Asp Leu Asp Tyr Lys Asp Asp Asp Lys Leu Ala His Thr His Gln			
385	390	395	400
Asp Phe Gln Pro Val Leu His Leu Val Ala Leu Asn Thr Pro Leu Ser			
405	410	415	
Gly Gly Met Arg Gly Ile Arg Gly Ala Asp Phe Gln Cys Phe Gln Gln			
420	425	430	
Ala Arg Ala Val Gly Leu Ser Gly Thr Phe Arg Ala Phe Leu Ser Ser			
435	440	445	

Arg Leu Gln Asp Leu Tyr Ser Ile Val Arg Arg Ala Asp Arg Gly Ser  
 450 455 460  
 Val Pro Ile Val Asn Leu Lys Asp Glu Val Leu Ser Pro Ser Trp Asp  
 465 470 475 480  
 Ser Leu Phe Ser Gly Ser Gln Gly Gln Val Gln Pro Gly Ala Arg Ile  
 485 490 495  
 Phe Ser Phe Asp Gly Arg Asp Val Leu Arg His Pro Ala Trp Pro Gln  
 500 505 510  
 Lys Ser Val Trp His Gly Ser Asp Pro Ser Gly Arg Arg Leu Met Glu  
 515 520 525  
 Ser Tyr Cys Glu Thr Trp Arg Thr Glu Thr Thr Gly Ala Thr Gly Gln  
 530 535 540  
 Ala Ser Ser Leu Leu Ser Gly Arg Leu Leu Glu Gln Lys Ala Ala Ser  
 545 550 555 560  
 Cys His Asn Ser Tyr Ile Val Leu Cys Ile Glu Asn Ser Phe Met Thr  
 565 570 575  
 Ser Phe Ser Lys  
 580

<210> 17  
 <211> 549  
 <212> DNA  
 <213> Homo sapiens

<400> 17  
 cacagccacc ggcacttcca gccggtgctc cacctgggtg cgctcaacag cccctgtca 60  
 ggccgcatgc ggggcatccg cggggccgac ttccagtgtt tccagcaggc gcgggcccgtg 120  
 gggctggcgg gcaccttccg cgccttcctg tcctcgcgcc tgcaggacct gtacagcatc 180  
 gtgcgccgtg ccgaccgcgc agccgtgccc atcgtcaacc tcaaggacga gctgctgttt 240  
 cccagctggg aggtctgtgt ctcaggctct gagggtcgc tgaagcccgg ggcacgcac 300  
 ttctcctttg acggcaagga cgtcctgagg caccctcacct ggccccagaa gacgtgtgg 360  
 catggctcgg accccaacgg gcgcaggctg accgagagct actgtgagac gtggcggacg 420  
 gaggctccct cggccacggg ccaggcctcc tcgtgctggt ggggcaggct cctggggcag 480  
 agtgccgcga gctgccatca cgcctacatc gtgctctgca ttgagaacag cttcatgact 540  
 gcctccaag 549

<210> 18  
 <211> 183  
 <212> PRT  
 <213> Homo sapiens

<400> 18  
 His Ser His Arg Asp Phe Gln Pro Val Leu His Leu Val Ala Leu Asn  
 1 5 10 15  
 Ser Pro Leu Ser Gly Gly Met Arg Gly Ile Arg Gly Ala Asp Phe Gln  
 20 25 30  
 Cys Phe Gln Gln Ala Arg Ala Val Gly Leu Ala Gly Thr Phe Arg Ala  
 35 40 45  
 Phe Leu Ser Ser Arg Leu Gln Asp Leu Tyr Ser Ile Val Arg Arg Ala  
 50 55 60  
 Asp Arg Ala Ala Val Pro Ile Val Asn Leu Lys Asp Glu Leu Leu Phe  
 65 70 75 80  
 Pro Ser Trp Glu Ala Leu Phe Ser Gly Ser Glu Gly Pro Leu Lys Pro  
 85 90 95  
 Gly Ala Arg Ile Phe Ser Phe Asp Gly Lys Asp Val Leu Arg His Pro

	100		105		110
Thr Trp	Pro Gln Lys Ser Val Trp	His Gly Ser Asp	Pro Asn Gly Arg		
	115	120	125		
Arg Leu	Thr Glu Ser Tyr Cys Glu	Thr Trp Arg Thr	Glu Ala Pro Ser		
	130	135	140		
Ala Thr	Gly Gln Ala Ser Ser Leu	Leu Gly Gly Arg	Leu Leu Gly Gln		
145	150	155	160		
Ser Ala	Ala Ser Cys His His Ala	Tyr Ile Val Leu	Cys Ile Glu Asn		
	165	170	175		
Ser Phe	Met Thr Ala Ser Lys				
	180				

<210> 19  
 <211> 5408  
 <212> DNA  
 <213> Homo sapiens

<400> 19

gcccgcgtcga	cgcggcggag	gaggcagcat	cccgcggcgc	tgacggtcct	ggggagagca	60
tggcgcggag	gtgcccctgg	ccatggccgc	ggcggcggcg	cctcctggac	gtgctcgcgc	120
ccctggctcct	gctgctcggg	gtccgcgcgg	cctccgcgga	gccagagcgc	atcagcggag	180
aggtggggct	gctgcagctc	cttggggacc	ccccgcccc	gcaggtcacc	cagacggatg	240
accccgacgt	cgggctggcc	tacgtctttg	ggccagatgc	caacagtggc	caagtggccc	300
ggtaccactt	ccccagcctc	ttcttccttg	acttctcact	gctgttccac	atccggccag	360
ccacagaggg	cccaggggtg	ctgttcgcca	tcacggactc	ggcgcaggcc	atggtcttgc	420
tgggcgtgaa	gctctctggg	gtgcaggacg	ggcaccagga	catctccctg	ctctacacag	480
aacctggtgc	aggccagacc	cacacagccg	ccagcttccg	gctccccgcc	ttcgtcggcc	540
agtggacaca	cttagccctc	agtgtggcag	gtggctttgt	ggccctctac	gtggactgtg	600
aggagtccca	gagaatgccg	cttgctcggg	cctcacgggg	cctggagctg	gagcctggcg	660
ccgggctctt	cgtggctcag	gcggggggag	cggaccctga	caagtccag	ggggtgatcg	720
ctgagctgaa	gggtgcgcag	gacccccagg	tgagccccat	gcactgcctg	gacgagggaag	780
gcatgactc	agatggggca	ttcggagact	ctggcagcgg	gctcggggac	gccccgggagc	840
ttctcaggga	ggagacgggc	gcggccctaa	aaccagggct	ccccgcgcca	ccccccgtca	900
ccacgccacc	cttggctgga	ggcagcagca	cgggaagattc	cagaagtga	gaagtgcagg	960
agcagaccac	ggtggcttcg	ttaggagctc	agacacttcc	tggtcagat	tctgtctcca	1020
cgtgggacgg	gagtgtcccg	acccctgggg	gccgcgtgaa	agagggcggc	ctgaaggggc	1080
agaaagggga	gccaggtggt	ccggggccac	ctggccgggc	aggcccccca	ggatccccat	1140
gcctacctgg	tccccggggt	ctcccggtgc	cagtgaagtc	cctgggtcct	gcaggcccag	1200
cgttgcaaac	tgtccccgga	ccacaaggac	ccccagggcc	tccggggagg	gacggcaccc	1260
ctggaaggga	cggcgagccg	ggcgaccccg	gtgaagacgg	aaagccgggc	gacaccgggc	1320
cacaaggctt	ccctgggact	ccaggggatg	taggtcccaa	gggagacaag	ggagaccctg	1380
gggttgagga	gagaggggcc	ccaggacccc	aagggcctcc	aggcccccca	ggaccctcct	1440
tcagacacga	caagctgacc	ttcattgaca	tggagggatc	tggctttggg	ggcgtatctg	1500
agggcctgcg	gggtcctcga	ggcttccttg	gacctcccg	accccccggt	gtcccaggcc	1560
tgcccggcga	gccaggccgc	tttggggtga	acagctccga	cgtcccagga	cccgcgggcc	1620
ttcctggtgt	gcctggggcg	gagggtcccc	ccgggtttcc	tggcctcccc	ggacccccag	1680
gccctccggg	aagagagggg	cccccaggaa	ggactgggca	gaaaggcagc	ctgggtgaag	1740
caggcgcccc	aggacataag	gggagcaagg	gagcccccg	tctgctggt	gctcgtgggg	1800
agagcggcct	ggcaggagcc	cccggacctg	ctggaccacc	aggccccct	gggccccctg	1860
ggcccccagg	accaggactc	cccgtggat	ttgatgacat	ggaaggctcc	ggggggccct	1920
tctggtcaac	agcccgaagc	gctgatgggc	cacagggacc	tcccggcctg	ccgggactta	1980
agggggatcc	tggcgtgcct	gggctgcccg	gggcgaaggg	agaagttgga	gcagatggaa	2040
tccccgggtt	ccccggcctc	cctggcagag	agggcattgc	tgggccccag	gggccaagg	2100
gagacagagg	cagccgggga	gaaaagggag	atccagggaa	ggacggagtc	gggcagccgg	2160
gcctccctgg	cccccccgga	cccccgggac	ctgtggtcta	cgtgtcggag	caggacggat	2220

ccgtcctgag	cgtgccggga	cctgagggcc	ggccgggttt	cgcaggcttt	cccggacctg	2280
caggacccaa	gggcaacctg	ggctctaagg	gcgaacgagg	ctccccggga	cccaagggtg	2340
agaagggtga	accgggcagc	atcttcagcc	ccgacggcgg	tgccctgggc	cctgcccaga	2400
aaggagccaa	gggagagccg	ggcttcagag	gacccccggg	tccatacggg	cggccggggt	2460
acaaggaggga	gattggcttt	cctggacggc	cggttcgccc	cgggatgaac	ggattgaaaag	2520
gagagaaaag	ggagccggga	gatgccagcc	ttggatttgg	catgagggga	atgcccgcc	2580
ccccaggacc	tccaggggcc	ccaggccctc	cagggaactc	tgtttacgac	agcaatgtgt	2640
ttgctgagtc	cagccgcccc	gggcctccag	gattgccagg	gaatcagggc	cctccaggac	2700
ccaaggggcg	caaaggagaa	gtggggcccc	ccggaccacc	agggcagttt	ccgtttgact	2760
ttcttcagtt	ggaggctgaa	atgaaggggg	agaagggaga	ccgaggtgat	gcaggacaga	2820
aaggcgaaaag	gggggagccc	gggggcggcg	gtttcttcgg	ctccagcctg	cccggccccc	2880
ccggccccc	aggcccacgt	ggctaccctg	ggattccagg	tccaaggga	gagagcatcc	2940
ggggccagcc	cggcccacct	ggacctcagg	gaccccccg	catcggctac	gaggggcgcc	3000
agggcctcc	cggccccc	ggcccccag	ggcccccctc	attcctggc	cctcacaggc	3060
agactatcag	cgttccccgg	cctccggggc	ccccggggc	ccctggggcc	cctggaacca	3120
tgggcgcctc	ctcagggttg	aggctctggg	ctacacgcca	ggccatgctg	ggccagggtc	3180
acgagggttc	cgagggttgg	ctcatcttcg	tggccgagca	ggaggagctc	tacgtccgcg	3240
tgcagaacgg	gttccggaag	gtccagctgg	aggcccggac	accactccca	cgagggacgg	3300
acaatgaagt	ggccgccttg	cagccccccg	tggtgcagct	gcacgacagc	aaccctacc	3360
cgcggcgggg	gcacccccac	cccaccgcgc	ggccctggcg	ggcagatgac	atcctggcca	3420
gccccctcg	cctgcccag	ccccagccct	accccgagc	cccgaccac	agctcctacg	3480
tgcacctgcg	gccggcgcg	cccacaagcc	caccgcacca	cagccaccgc	gacttccagc	3540
cgggtgctcca	cctgggttgcg	ctcaacagcc	ccctgtcagg	cggcatgcgg	ggcatccgcg	3600
ggggccgactt	ccagtgcctt	cagcaggcgc	ggggcgtggg	gctggcgggc	accttccgcg	3660
ccttctctgtc	ctcgcgcctg	caggacctgt	acagcatcgt	gcgcgtgcc	gaccgcgacg	3720
ccgtgcccc	cgtcaacctc	aaggacgagc	tgtgttttcc	cagctgggag	gctctgttct	3780
caggctctga	gggtccgctg	aagcccgggg	cacgcatctt	ctcctttgac	ggcaaggacg	3840
tcctgaggca	ccccacctgg	ccccagaaga	gcgtgtggca	tggctcggac	cccaacgggc	3900
gcaggctgac	cgagagctac	tgtgagacgt	ggcggacgga	ggctccctcg	gccacgggccc	3960
aggcctcctc	gctgtggggg	ggcaggctcc	tggggcagag	tgcccgagc	tgccatcacg	4020
cctacatcgt	gctctgcatt	gagaacagct	tcatactgc	ctccaagtag	ccaccgcctg	4080
gatgcggtg	gccggagagg	accggcggtc	cggagggaagc	ccccaccgtg	ggcaggggagc	4140
ggccggccag	cccctggccc	caggacctgg	ctgccatact	ttcctgtata	gttcacgttt	4200
catgtaatcc	tcaagaaata	aaagggaagc	aaagagtgtg	tttttttaaa	agtttaaaac	4260
agaagcctga	tgctgacatt	cacctgcccc	aactctcccc	tgacctgtga	gcccagctgg	4320
gtcaggcgagg	gtgcagtatc	atgcctctgt	caacctcttg	gcctgatcag	accacggctc	4380
gatttctcca	ggatttccctg	ctttgggaag	ccgtgctcgc	cccagcaggt	gctgacttca	4440
tctccacact	agcagcaccg	ttctgtgcac	aaaacccaga	cctgttagca	gacaggcccc	4500
gtgaggcaat	gggagctgag	gccacactca	gcacaaggcc	atctgggctc	ctccagggtg	4560
tgtgctcgcc	ctgcggtaga	tgggagggag	gctcaggctc	ctggggctag	ggggagcccc	4620
ttctgctcag	ctctggggcca	ttctccacag	caaccccagg	ctgaagcagg	ttcccaagct	4680
cagaggcgca	ctgtgacccc	cagctccggc	ctgtcctcca	acaccaagca	cagcagcctg	4740
gggctggcct	cccaaatgag	ccatgagatg	atacatccaa	agcagacagc	tccaccctgg	4800
ccgagtccaa	gctgggagat	tcaagggacc	catgagttgg	ggtctggcag	cctcccatcc	4860
aggggcccca	tctcatgccc	ctggctggga	cgtggctcag	ccagcacttg	tccagctgag	4920
cgccaggatg	gaacacggcc	acatcaaaga	ggctgaggct	ggcacaggac	atgcggtagc	4980
cagcacacag	ggcagtgagg	gagggtctgt	atctgtgcac	tgcccatgga	caggctggct	5040
ccagatgcag	ggcagtcatt	ggctgtctcc	taggaacccc	atatccttac	cctccttggg	5100
actgaagggg	aaccccgggg	tgcccacagg	ccgcctcgcg	ggtgaacaaa	gcagccacga	5160
ggtgcaacaa	ggtcctctgt	cagtcacagc	cacccctgag	atccggcaac	atcaacccga	5220
gtcattcgtt	ctgtggaggg	acaagtggac	tcagggcagc	gccaggctga	ccacagcaca	5280
gccaacacgc	acctgcctca	ggactgcgac	gaaaccgggtg	gggctgggtc	tgtaattgtg	5340
tgtagtgtga	agccaattca	gacaggcaaa	taaaagtgcac	cttttacct	gaaaaaaaaa	5400
aaaaaaaa						5408

<210> 20  
 <211> 1336  
 <212> PRT  
 <213> Homo sapiens

<400> 20  
 Met Ala Pro Arg Cys Pro Trp Pro Trp Pro Arg Arg Arg Arg Leu Leu  
 1 5 10 15  
 Asp Val Leu Ala Pro Leu Val Leu Leu Leu Gly Val Arg Ala Ala Ser  
 20 25 30  
 Ala Glu Pro Glu Arg Ile Ser Glu Glu Val Gly Leu Leu Gln Leu Leu  
 35 40 45  
 Gly Asp Pro Pro Pro Gln Gln Val Thr Gln Thr Asp Asp Pro Asp Val  
 50 55 60  
 Gly Leu Ala Tyr Val Phe Gly Pro Asp Ala Asn Ser Gly Gln Val Ala  
 65 70 75 80  
 Arg Tyr His Phe Pro Ser Leu Phe Phe Arg Asp Phe Ser Leu Leu Phe  
 85 90 95  
 His Ile Arg Pro Ala Thr Glu Gly Pro Gly Val Leu Phe Ala Ile Thr  
 100 105 110  
 Asp Ser Ala Gln Ala Met Val Leu Leu Gly Val Lys Leu Ser Gly Val  
 115 120 125  
 Gln Asp Gly His Gln Asp Ile Ser Leu Leu Tyr Thr Glu Pro Gly Ala  
 130 135 140  
 Gly Gln Thr His Thr Ala Ala Ser Phe Arg Leu Pro Ala Phe Val Gly  
 145 150 155 160  
 Gln Trp Thr His Leu Ala Leu Ser Val Ala Gly Gly Phe Val Ala Leu  
 165 170 175  
 Tyr Val Asp Cys Glu Glu Phe Gln Arg Met Pro Leu Ala Arg Ser Ser  
 180 185 190  
 Arg Gly Leu Glu Leu Glu Pro Gly Ala Gly Leu Phe Val Ala Gln Ala  
 195 200 205  
 Gly Gly Ala Asp Pro Asp Lys Phe Gln Gly Val Ile Ala Glu Leu Lys  
 210 215 220  
 Val Arg Arg Asp Pro Gln Val Ser Pro Met His Cys Leu Asp Glu Glu  
 225 230 235 240  
 Gly Asp Asp Ser Asp Gly Ala Phe Gly Asp Ser Gly Ser Gly Leu Gly  
 245 250 255  
 Asp Ala Arg Glu Leu Leu Arg Glu Glu Thr Gly Ala Ala Leu Lys Pro  
 260 265 270  
 Arg Leu Pro Ala Pro Pro Pro Val Thr Thr Pro Pro Leu Ala Gly Gly  
 275 280 285  
 Ser Ser Thr Glu Asp Ser Arg Ser Glu Glu Val Glu Glu Gln Thr Thr  
 290 295 300  
 Val Ala Ser Leu Gly Ala Gln Thr Leu Pro Gly Ser Asp Ser Val Ser  
 305 310 315 320  
 Thr Trp Asp Gly Ser Val Arg Thr Pro Gly Gly Arg Val Lys Glu Gly  
 325 330 335  
 Gly Leu Lys Gly Gln Lys Gly Glu Pro Gly Val Pro Gly Pro Pro Gly  
 340 345 350  
 Arg Ala Gly Pro Pro Gly Ser Pro Cys Leu Pro Gly Pro Pro Gly Leu  
 355 360 365  
 Pro Cys Pro Val Ser Pro Leu Gly Pro Ala Gly Pro Ala Leu Gln Thr  
 370 375 380

Val Pro Gly Pro Gln Gly Pro Pro Gly Pro Pro Gly Arg Asp Gly Thr  
 385 390 395 400  
 Pro Gly Arg Asp Gly Glu Pro Gly Asp Pro Gly Glu Asp Gly Lys Pro  
 405 410 415  
 Gly Asp Thr Gly Pro Gln Gly Phe Pro Gly Thr Pro Gly Asp Val Gly  
 420 425 430  
 Pro Lys Gly Asp Lys Gly Asp Pro Gly Val Gly Glu Arg Gly Pro Pro  
 435 440 445  
 Gly Pro Gln Gly Pro Pro Gly Pro Gly Pro Ser Phe Arg His Asp  
 450 455 460  
 Lys Leu Thr Phe Ile Asp Met Glu Gly Ser Gly Phe Gly Gly Asp Leu  
 465 470 475 480  
 Glu Ala Leu Arg Gly Pro Arg Gly Phe Pro Gly Pro Pro Gly Pro Pro  
 485 490 495  
 Gly Val Pro Gly Leu Pro Gly Glu Pro Gly Arg Phe Gly Val Asn Ser  
 500 505 510  
 Ser Asp Val Pro Gly Pro Ala Gly Leu Pro Gly Val Pro Gly Arg Glu  
 515 520 525  
 Gly Pro Pro Gly Phe Pro Gly Leu Pro Gly Pro Gly Pro Pro Gly  
 530 535 540  
 Arg Glu Gly Pro Pro Gly Arg Thr Gly Gln Lys Gly Ser Leu Gly Glu  
 545 550 555 560  
 Ala Gly Ala Pro Gly His Lys Gly Ser Lys Gly Ala Pro Gly Pro Ala  
 565 570 575  
 Gly Ala Arg Gly Glu Ser Gly Leu Ala Gly Ala Pro Gly Pro Ala Gly  
 580 585 590  
 Pro Pro Gly Pro Pro Gly Pro Pro Gly Pro Pro Gly Pro Gly Leu Pro  
 595 600 605  
 Ala Gly Phe Asp Asp Met Glu Gly Ser Gly Gly Pro Phe Trp Ser Thr  
 610 615 620  
 Ala Arg Ser Ala Asp Gly Pro Gln Gly Pro Pro Gly Leu Pro Gly Leu  
 625 630 635 640  
 Lys Gly Asp Pro Gly Val Pro Gly Leu Pro Gly Ala Lys Gly Glu Val  
 645 650 655  
 Gly Ala Asp Gly Ile Pro Gly Phe Pro Gly Leu Pro Gly Arg Glu Gly  
 660 665 670  
 Ile Ala Gly Pro Gln Gly Pro Lys Gly Asp Arg Gly Ser Arg Gly Glu  
 675 680 685  
 Lys Gly Asp Pro Gly Lys Asp Gly Val Gly Gln Pro Gly Leu Pro Gly  
 690 695 700  
 Pro Pro Gly Pro Pro Gly Pro Val Val Tyr Val Ser Glu Gln Asp Gly  
 705 710 715 720  
 Ser Val Leu Ser Val Pro Gly Pro Glu Gly Arg Pro Gly Phe Ala Gly  
 725 730 735  
 Phe Pro Gly Pro Ala Gly Pro Lys Gly Asn Leu Gly Ser Lys Gly Glu  
 740 745 750  
 Arg Gly Ser Pro Gly Pro Lys Gly Glu Lys Gly Glu Pro Gly Ser Ile  
 755 760 765  
 Phe Ser Pro Asp Gly Gly Ala Leu Gly Pro Ala Gln Lys Gly Ala Lys  
 770 775 780  
 Gly Glu Pro Gly Phe Arg Gly Pro Pro Gly Pro Tyr Gly Arg Pro Gly  
 785 790 795 800  
 Tyr Lys Gly Glu Ile Gly Phe Pro Gly Arg Pro Gly Arg Pro Gly Met  
 805 810 815  
 Asn Gly Leu Lys Gly Glu Lys Gly Glu Pro Gly Asp Ala Ser Leu Gly

820 825 830  
 Phe Gly Met Arg Gly Met Pro Gly Pro Pro Gly Pro Pro Gly Pro Pro  
 835 840 845  
 Gly Pro Pro Gly Thr Pro Val Tyr Asp Ser Asn Val Phe Ala Glu Ser  
 850 855 860  
 Ser Arg Pro Gly Pro Pro Gly Leu Pro Gly Asn Gln Gly Pro Pro Gly  
 865 870 875 880  
 Pro Lys Gly Ala Lys Gly Glu Val Gly Pro Pro Gly Pro Pro Gly Gln  
 885 890 895  
 Phe Pro Phe Asp Phe Leu Gln Leu Glu Ala Glu Met Lys Gly Glu Lys  
 900 905 910  
 Gly Asp Arg Gly Asp Ala Gly Gln Lys Gly Glu Arg Gly Glu Pro Gly  
 915 920 925  
 Gly Gly Gly Phe Phe Gly Ser Ser Leu Pro Gly Pro Pro Gly Pro Pro  
 930 935 940  
 Gly Pro Arg Gly Tyr Pro Gly Ile Pro Gly Pro Lys Gly Glu Ser Ile  
 945 950 955 960  
 Arg Gly Gln Pro Gly Pro Pro Gly Pro Gln Gly Pro Pro Gly Ile Gly  
 965 970 975  
 Tyr Glu Gly Arg Gln Gly Pro Pro Gly Pro Pro Gly Pro Pro Gly Pro  
 980 985 990  
 Pro Ser Phe Pro Gly Pro His Arg Gln Thr Ile Ser Val Pro Gly Pro  
 995 1000 1005  
 Pro Gly Pro Pro Gly Pro Pro Gly Pro Pro Gly Thr Met Gly Ala Ser  
 1010 1015 1020  
 Ser Gly Val Arg Leu Trp Ala Thr Arg Gln Ala Met Leu Gly Gln Val  
 1025 1030 1035 104  
 His Glu Val Pro Glu Gly Trp Leu Ile Phe Val Ala Glu Gln Glu Glu  
 1045 1050 1055  
 Leu Tyr Val Arg Val Gln Asn Gly Phe Arg Lys Val Gln Leu Glu Ala  
 1060 1065 1070  
 Arg Thr Pro Leu Pro Arg Gly Thr Asp Asn Glu Val Ala Ala Leu Gln  
 1075 1080 1085  
 Pro Pro Val Val Gln Leu His Asp Ser Asn Pro Tyr Pro Arg Arg Glu  
 1090 1095 1100  
 His Pro His Pro Thr Ala Arg Pro Trp Arg Ala Asp Asp Ile Leu Ala  
 1105 1110 1115 112  
 Ser Pro Pro Arg Leu Pro Glu Pro Gln Pro Tyr Pro Gly Ala Pro His  
 1125 1130 1135  
 His Ser Ser Tyr Val His Leu Arg Pro Ala Arg Pro Thr Ser Pro Pro  
 1140 1145 1150  
 Ala His Ser His Arg Asp Phe Gln Pro Val Leu His Leu Val Ala Leu  
 1155 1160 1165  
 Asn Ser Pro Leu Ser Gly Gly Met Arg Gly Ile Arg Gly Ala Asp Phe  
 1170 1175 1180  
 Gln Cys Phe Gln Gln Ala Arg Ala Val Gly Leu Ala Gly Thr Phe Arg  
 1185 1190 1195 120  
 Ala Phe Leu Ser Ser Arg Leu Gln Asp Leu Tyr Ser Ile Val Arg Arg  
 1205 1210 1215  
 Ala Asp Arg Ala Ala Val Pro Ile Val Asn Leu Lys Asp Glu Leu Leu  
 1220 1225 1230  
 Phe Pro Ser Trp Glu Ala Leu Phe Ser Gly Ser Glu Gly Pro Leu Lys  
 1235 1240 1245  
 Pro Gly Ala Arg Ile Phe Ser Phe Asp Gly Lys Asp Val Leu Arg His  
 1250 1255 1260

Pro Thr Trp Pro Gln Lys Ser Val Trp His Gly Ser Asp Pro Asn Gly  
1265 1270 1275 128  
Arg Arg Leu Thr Glu Ser Tyr Cys Glu Thr Trp Arg Thr Glu Ala Pro  
1285 1290 1295  
Ser Ala Thr Gly Gln Ala Ser Ser Leu Leu Gly Gly Arg Leu Leu Gly  
1300 1305 1310  
Gln Ser Ala Ala Ser Cys His His Ala Tyr Ile Val Leu Cys Ile Glu  
1315 1320 1325  
Asn Ser Phe Met Thr Ala Ser Lys  
1330 1335



## INTERNATIONAL SEARCH REPORT

 International application No.  
 PCT/US98/24950

<b>A. CLASSIFICATION OF SUBJECT MATTER</b> IPC(6) : A01N 63/00; 43/04; C12N 15/00; C07H 21/02 US CL : 424/93.1; 435/320.1; 514/44; 536/23.1 According to International Patent Classification (IPC) or to both national classification and IPC		
<b>B. FIELDS SEARCHED</b> Minimum documentation searched (classification system followed by classification symbols) U.S. : 424/93.1; 435/320.1; 514/44; 536/23.1 Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched Electronic data base consulted during the international search (name of data base and, where practicable, search terms used) Please See Extra Sheet.		
<b>C. DOCUMENTS CONSIDERED TO BE RELEVANT</b>		
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y,P	US 5,792,845 A (O'REILLY et al.) 11 August 1998 (11.08.98), col. 4, lines 32-68, col. 5, lines 1-2, 51-68, col. 6, lines 1-8.	1-30, 33
Y	WO 97/23500 A1 (THE CHILDREN'S MEDICAL CENTER CORPORATION) 03 July 1997 (03.07.97), page 41, lines 3-33, page 42, lines 1-27.	4
X,P	WO 98/49321 A2 (RHONE-POULENC RORER) 05 November 1998 (05.11.98), page 44, 6-11, 25-33, page 45, lines 12-13, 29-35.	1, 5, 18, 20, 31
Y,P		2-4, 6-17, 19, 21-30, 32, 33
<input checked="" type="checkbox"/> Further documents are listed in the continuation of Box C. <input type="checkbox"/> See patent family annex.		
* Special categories of cited documents: *A* document defining the general state of the art which is not considered to be of particular relevance *E* earlier document published on or after the international filing date *L* document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified) *O* document referring to an oral disclosure, use, exhibition or other means *P* document published prior to the international filing date but later than the priority date claimed *T* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention *X* document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone *Y* document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art *Z* document member of the same patent family		
Date of the actual completion of the international search 04 FEBRUARY 1999		Date of mailing of the international search report 08 MAR 1999
Name and mailing address of the ISA/US Commissioner of Patents and Trademarks Box PCT Washington, D.C. 20231 Facsimile No. (703) 305-3230		Authorized officer SHIN-ERN CHEN Telephone No. (703) 308-0196

## INTERNATIONAL SEARCH REPORT

International application No.  
PCT/US98/24950

## C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	WO 97/15666 A (THE CHILDREN'S MEDICAL CENTER CORPORATION) 01 May 1997 (01.05.97), page 20, lines 16-35, page 21, page 22, lines 1-16. page 59, lines 5-35, page 60, page 61, 1-6.	1-30, 33
Y	TANAKA, T. et al. Retroviral and adenoviral mediated transduction of angiostatin cDNA inhibits angiogenesis and tumor growth. Proceedings of the American Association for Cancer Research. March 1997 (03.97). Vol 38. page 264.	1-33
Y	WO 96/35774 A2 (THE CHILDREN'S MEDICAL CENTER CORPORATION) 14 November 1996 (14.11.96), page lines 33-36, pages 22-25, page 26, lines 1-33. pages 144-148.	1-30, 33
Y	WO 97/41824 A2(ABBOTT LABORATORIES) 13 November 1997 (13.11.97), page 5, lines 13-38, page 6, 1-18, page 60, lines 15-38, pages 61-62, page 63, lines 1-33.	1-30, 33
Y	WO 95/29242 A1 (THE CHILDREN'S MEDICAL CENTER CORPORATION) 02 November 1995 (02.11.95), page 21, lines 19-35, pages 22-27, page 28, lines 1-4. page 87, lines 4-35, page 88, page 89, lines 1-14.	1-30, 33
Y	O'REILLY, et al. Angiostatin induces and sustains dormancy of human primary tumors in mice. Nature Medicine, June 1996 (06.96), Vol. 2, No. 6, pages 689-692, especially pages 689-690.	1-30, 33
Y	O'REILLY, et al. Endostatin: An Endogenous Inhibitor of Angiogenesis and Tumor Growth. Cell, 24 January 1997 (24.01.97), Vol. 88, pages 277-285, especially pages 279-280, 282.	1-30, 33

## INTERNATIONAL SEARCH REPORT

International application No.

PCT/US98/24950

### B. FIELDS SEARCHED

Electronic data bases consulted (Name of data base and where practicable terms used):

APS, STN, WPIDS, MEDLINE, CAPLUS, BIOSIS, EMBASE

search terms: angiostatin, plasminogen, endostatin, collagen(w) XVIII, inhibit?(5a)tumor(5a)growth, tumor(5a)regress?, diabet?(p)retinopathy, plasmid, viral(5a) vector.